

FIGURE 1A

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	1 TACCAAGTGC GCAACTCCACGGGGCTTTACCATGTtACCAATGATTGCCCTAACTCGAGTA
1	DK7	1 TACCAAGTGC GCAACTCCACGGGGCTTTACCATGTcACCAATGATTGCCCTAACTCGAGTA
9	US11	1 TACCAAGTaCGCAACTCCACGGGGCTTTACCATGTcACCAATGATTGCCCTAACTCGAGTA
4	DR4	1 CACCAAGTGC GCAACTCTACAGGGCTTTACCATGTcACCAATGATTGCCCTAATTTCGAGTA
3	DR1	1 CACCAAGTGC GCAACTCTACAGGGCTTTACCATGTcACCAATGATTGCCCTAATTTCGAGTA
2	DK9	1 TACCAAGTACGCAACTCCtCGGGCCTcTACCATGTcACCAATGATTGCCCTAACTCGAGTA
6	S18	1 TACCAAGTACGCAACTCCaCGGGCCTTTACCATGTcACCAATGAcTGCCCTAACTCGAGcA
7	SW1	1 TACCAAGTACGCAACTCCtCGGGCCTTTACCATGTcACCAATGAcTGCCCTAACTCGAGtA
1-8	consensus	tACCAAGT - CGCAACTCcaCgGGGcCTtTACCATGTcACCAATGAcTGCCCTAAcTCGAGtA

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	62 TtGTGTACGAGaCaGcTgATGcTATCCTaCACgCTCCGGGaTGTGTCCCTTGCGTTcGtGA
1	DK7	62 TcGTGTACGAGGCGGCCGATGCCATCCTGCACACTCCGGGGTGTGTCCCTTGCGTTcGCGA
8	US11	62 TTGTGTACGAGGCGGCCGATGCCATCCTGCACACTCCGGGGTGTGTtCCTTGCGTTcGCGA
4	DR4	62 TTGTGTACGAGGCGGCCGATGCCATCCTGCACAGCCGGGGTGTGTCCCTTGCGTTcGCGA
3	DR1	62 TTGTGTACGAGGCGGCCGATGCCATCCTGCACgCGCCGGGGTGTGTCCCTTGCGTTcGCGA
2	DK9	62 TTGTGTACGAGGCGGCCGATGCCATCCTGCAtTCTCCaGGGTGTGTCCCTTGCGTTcGCGA
6	S18	62 TTGTGTACGAGACGGCCGATaCCATcCTACACTCTCCgGGGTGTGTCCCTTGCGTTcGCGA
7	SW1	62 TTGTGTACGAGACGGCCGATgCCATtCTACACTCTCCaGGGTGTGTCCCTTGCGTTcGCGA
1-8	consensus	TtGTGTACGAGgCgGCCGATgCcATcCTgCAc - CtCCgGGgTGTGTcCCTTGCGTTcGcGA

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	123 GGGTAACacCTCGAGGTGTTGGGTGGCGATGACCCCCACGGTGGCCACCAGGGAcGGCAAA
1	DK7	123 GGGTAACGtCTCGAGGTGTTGGGTGGCGATGACCCCCACGGTGGCCACCAGGGAtGGCAAA
8	US11	123 GGGTAACGcTTCGAGGTGTTGGGTGGCGATGACCCCCACGGTGGCCACCAGGGACGGCAAA
4	DR4	123 GGGTAACaCCTCGAGGTGTTGGGTGGCGGTGACCCCCACGGTGGCCACCAGGGACGGCAAA
3	DR1	123 GGGTAACGCCTCGAGGTGTTGGGTGGCGGTGACCCCCACGGTGGCCACCAGGGACGGCAAA
2	DK9	123 GGGTAACGCCTCGAaATGTTGGGTGGCGGTGGCCCCACGGTGGCCACCAGGGACGGCAAg
6	S18	123 GGGTAACGCCTCGAgATGTTGGGTGcCGGTGGCCCCCACAGTtGCCACCAGGGACGGCAAA
7	SW1	23 GGATggCGCCcCGAagTGTTGGGTGgCGGTGGCCCCCACAGTcGCCAcTAGGGACGGCAAA
1-8	consensus	GGgTaaCgcctCGAggTGTTGGGTGgCGgTGaCCCCCACgGTgGCCACcAGGGAcGGCAaa

FIGURE 1A

SEQ ID NO:	Isolate	Sequence
5	S14	184 CTCCCCgCAaCGCAGCTTCGACGTtACATCGATCTGCTtGTCGGGAGcGCCACCCTCTGTT
1	DK7	184 CTCCCCACAgCGCAGCTTCGACGTcACATCGATCTGCTcGTCGGGAGtGCCACCCTCTGTT
8	US11	184 CTCCCCACAACGCAaCTTCGACGTcACATCGATCTGCTTGTcGGGAGCGCCACCCTCTGTT
4	DR4	184 CTCCCCACAACGCGAGCTcCGACGTcACATCGACCTGCTTGTcGGGAGCGCCACCCTCTGCT
3	DR1	184 CTCCCCACAACGCGAGCTTCGACGTcACATCGACCTGCTTGTcGGGAGCGCCACCCTCTGCT
2	DK9	184 CTCCCCGCAACGCGAGCTTCGACGTcACATCGATCTGCTTGTcGGGAGCGCCACCCTCTGCT
6	S18	184 CTCCCCGCAACGCGAGCTTCGACGTcACATCGATCTGCTTGTtGGGAGCGCCACCCTCTGCT
7	SW1	184 CTCCCTtGCAACGCGAGCTTCGACGTcACATCGATCTGCTTGTtGGaAGCGCCACCCTCTGCT
1-8	consensus	CTCCCCc-CAaCGCAgCTtCGACGTcACATCGAtCTGCTtGTcGGgAGcGCCACCCTCTGcT

SEQ ID NO:	Isolate	Sequence
5	S14	245 CGGCCCTCTACGTGGGGGACtTGTGCGGGTCTGTCTTTCTTGTcGGTCAgCTGTTTACCTT
1	DK7	245 CGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTTCTTGTcGGTCAACTGTTTACCTT
8	S11	245 CGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTTCTTGTcGGTCAACTGTTTACCTT
4	DR4	245 CGGCCCTCTACGTGGGGGACtTGTGCGGGTCTGTCTTCTTGTcGGTCAACTGTTTACCTT
3	DR1	245 CGGCCCTCTACGTGGGGGACcTGTGCGGGTCTGTCTTCTTGTcGGTCAACTGTTTACCTT
2	DK9	245 CGGCCCTCTATGTGGGGGACtTGTGCGGGTCTGTCTTCTTGTcGGCCAAGTGTTCACCTT
6	S18	245 CGGCCCTCTATGTGGGGGACcTGTGCGGGTCTGTCTTTCTTGTcAGCCAgCTGTTCACTaT
7	SW1	245 CGGCCCTCTAcGTGGGGGACtTGTGCGGGTCTGTCTTTCTcGTcAGtCAaCTGTTCACTgtT
1-8	consensus	CGGCCCTCTAcGTGGGGGAC-TGTGCGGGTCTGTCTTtCTtGTcGgGtCAaCTGTTcACctT

SEQ ID NO:	Isolate	Sequence
5	S14	306 CTCTCCCAGGCGCCtCTGGACGACGCAAGaCTGCAATTGTTCTATCTATCCcGGCCATATA
1	DK7	306 CTCTCCCAGGCGCCACTGGACGACGCAAGGCTGCAATTGTTCTATCTATCCtGGCCATATA
8	S11	306 CTCTCCCAGaCGCCACTGGACGACGCAgGGCTGCAATTGTTCTATCTATCCCGGCCATATA
4	DR4	306 CTCTCCCAGGCaCCACTGGACAACGCAAGACTGCAATTGTTcATCTATCCCGGCCATATA
3	DR1	306 tTCTCCCAGGCGCCACTGGACAACGCAAGACTGCAATTGTTCTATCTATCCCGGCCATATA
2	DK9	306 CTCCCCAGaCGCCACTGGACAACGCAAGACTGCAACTGTTCTATCTATCCCCGGCCATAt
6	S18	306 CTCCCCAGGCGCCACTGGACAACGCAAGACTGCAACTGTTCTATCTATCCCCGGCCATATA
7	SW1	306 CTCCCCAGGCGCCACTGGACAACGCAAGACTGtAACTGTTCTATCTAtCCCCGGCCAcATA
1-8	consensus	cTCTcCCCAGgCgCCaCTGGACaACGCAaGaCTGcAAtTGTTCTATCTAtCCcGGCCAtATA

FIGURE 1A

SEQ ID NO:	Isolate	Sequence
5	S14	367 ACGGGTCatCGCATGGCaTGGGATATGATGATGAACTGGTCCCCTACgACGGCaCTGGTAG
1	DK7	367 ACGGGTCACCGCATGGCgTGGGATATGATGATGAACTGGTCCCCTACcACGGCGTTGGTAG
8	S11	367 ACGGGTCACCGCATGGCaTGGGATATGATGATGAACTGGTCCCCTACGgCGGCGTTGGTgG
4	DR4	367 ACGGGcCACCGCATGGCgTGGGATATGATGATGAACTGGTCCCCTACGACAGCGCTGGTAG
3	DR1	367 ACGGGaCACCGtATGGCaTGGGATATGATGATGAACTGGTCCCCTACGACAGCGCTGGTAA
2	DK9	367 ACGGGTCatCGcATGGCgTGGGATATGATGATGAACTGGTCCCCTACAgCAGCGCTGGTAA
6	S18	367 ACGGGTCACCGtATGGCATGGGATATGATGATGAACTGGTCCCCTACAACgGCGtTGGTAA
7	SW1	367 ACGGGTCACCGcATGGCATGGGATATGATGATGAACTGGTCCCCcACAACaGCGcTGGTAG
1-8	consensus	ACGGGtCacCGcATGGCaTGGGATATGATGATGAACTGGTCCCCTACgaC-GCgcTGGTag

SEQ ID NO:	Isolate	Sequence
5	S14	428 TAGCTCAGCTGCTCCGGATCCCcCAAGCCATCTTGGaLATGATCGCTGGTGTCTACTGGGG
1	DK7	428 TAGCTCAGCTGCTCCGGATCCCgCAAGCCATCTTGGACATGATCGCTGGTGTCTACTGGGG
8	S11	428 TAGCTCAGCTGCTCCGGATCCCACAAGCCATCTTGGACATGATCGCTGGTGTCTACTGGGG
4	DR4	428 TAGCTCAGCTGCTCCGGATCCCACAAGCCATCTTGGACATGATCGCTGGTGTCTACTGGGG
3	DR1	428 TGGCTCAGCTGCTCCGGATCCCACAAGCCATCTTGGACATGATCGCTGGaGCCCACTGGGG
2	DK9	428 TGGCgCAGCTGCTCAGGATCCCGCAgGCCATCTTGGACATGATCGCTGGTGTCTACTGGGG
6	S18	428 TAGCTCAGCTGCTCAGGgTCCCGCAAGCCGTCTTGGACATGATCGCTGGTGTCTACTGGGG
7	SW1	428 TAGCTCAGCTGCTCAGGaTCCCGCAAGCCGTCTTGGACATGATCGCTGGTGTCTACTGGGG
1-8	consensus	TaGCTcAGCTGCTCcGGATCCC-CAaGCCaTCTTGGAcATGATCGCTGGtGCcCACTGGGG

SEQ ID NO:	Isolate	Sequence
5	S14	489 AGTCCTaGCGGGCATAGCGTATTTtTCCATGGTGGGgAACTGGGCGAAGGTCCTaGtGtG
1	DK7	489 AGTCCTgGCGGGCATAGCGTATTTtTCCATGGTGGGgAACTGGGCGAAGGTCCTGGTAGTG
8	S11	489 AGTCCTAGCGGGCATAGCGTATTTCTCCATGGTGGGgAACTGGGCGAAGGTCCTGGTAGTG
4	DR4	489 AGTCCTAGCGGGCATAGCGTATTTCTCCATGGTGGGgAACTGGGCGAAGGTCCTGGTAGTG
3	DR1	489 AGTCCTAGCGGGCATAGCGTATTTCTCCATGGTGGGgAACTGGGCGAAGGTCGTGGTAGTG
2	DK9	489 AGTCCTAGCGGGCATAGCGTATTTCTCCATGGTGGGgAACTGGGCGAAGGTCGTGGTgGTa
6	S18	489 AGTCCTAGCGGGCATAGCGTATTTCTCCATGGcGGGgAACTGGGCGAAGGTCCTGcTAGTG
7	SW1	489 AGTCCTAGCGGGCATAGCGTATTTCTCCATGGtGGGgAACTGGGCGAAGGTCCTGaTAGTG
1-8	consensus	AGTCCTaGCGGGCATAGCGTATTTtTCCATGGtGGGgAACTGGGCGAAGGTCcTgGtAGTg

FIGURE 1A

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	550 CTGCTGCTATTcGCCGGCGTtGACGCG 
1	DK7	550 CTGCTGCTATTTGCCGGCGTCGACGCG 
8	US11	550 CTGCTGCTATTTGCCGGCGTCGACGCG 
4	DR4	550 CTGTTGCTGTTTGCCGGCGTTGATGCG 
3	DR1	550 CTGTTGCTGTTTGCCGGCGTTGATGCG 
2	DK9	550 CTGTTGCTGTTTaCCGGCGTCGATGCG 
6	S18	550 CTGTTGCTGTTTgCCGGCGTCGATGCG 
7	SW1	550 CTGTTGCTGTTTtCCGGCGTCGATGCG 
1-8	consensus	CTGtTGCTgTTtgCCGGCGTcGAtGCG

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FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	1 TATGAAGTGC GCAACGTGTCCGGGgTGTACCAcGTCACaAACGACTGCTCCAACtCAAGCA
24	T10	1 TATGAAGTGC GCAACGTGTCCGGGaTGTACCAcGTCACgAACGACTGCTCCAACtCAAGCA
10	D3	1 TATGAAGTGC GCAACGTGTCCGGGGTGTACCAaGTCACcAaTGA CTGTTCCAACtCGAGCA
9	D1	1 TATGAAGTGC GCAACGTGTCCGGGGTGTACCAcGTCACGAACGACTGTTCCAACtCGAGCA
14	HK5	1 TATGAAGTGC GCAACGTGTCCGGGGTATACCAcGTCACGAACGACTGCTCCAACtCAAGCA
15	HK8	1 TATGAAGTGC GCAACGTGTCCGGGATATACCAcGTCACGAACGACTGCTCCAACtCAAGCA
12	HK3	1 TATGAAGTGC GCAACGTGTCCGGGATATACCAcGTCACGAACGACTGCTCCAACtCAAGCg
23	T3	1 TAcGAAGTGC GCAACGTGTCCGGGGTGTACcATGTCACGAACGACTGTTCCAACtCAAGCA
22	SW2	1 TATGAAGTGC GCAACGTGTCCGGGGTGTAtCATGTCACGAACGACTGTTCCAACtCAAGCA
17	IND8	1 TATGAgGTGC GCAACGTGTCCGGGGTGTACCAcGTCACGAACGACTGCTCCAACtCAAGTA
16	IND5	1 TATGAAGTGC GCAACGTGTCCGGGGTGTACCAcGTCACGAACGACTGCTCCAACtCAAGTA
21	SA10	1 TATGAAGTGC GCAACGTGTCCGGGaTGTACCAcGTCACGAACGACTGCTCCAACtCAAGCA
20	S45	1 TATGAAGTGC GCAACGTGTCCGGGgcGTACCAcGTCACGAACGACTGCTCCAACtCAAGCA
25	US6	1 TATGAAGTGC GCAACGTGTCCGGGATGTACCAcGTCACGAACGACTGCTCCAACtCAAGCA
13	HK4	1 cATGAAGTGCaCAACGTaTCCGGGATcTACCAcGTCACGAACGACTGCTCCAACtCAAGTA
18	P10	1 TATGAAGTGC GCAACGTgTCCGGGGTGTACCAcGTCACGAACGACTGCTCCAACtCAAGTA
19	S9	1 TATGAAGTGC GCAACGTaTCCGGGGcGTACCAcGTCACGAACGACTGCTCCAACtCAAGTA
9-25	consensus	tAtGAaGTGCgCAACGTgTCCGGGgtgTAccAtGTCACgAAcGACTGcTCCAACtcaAGca

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FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	62 TcGTGTaTGAGGCAGtGGACgTGATCATGCAtACCCCaGGGTGCGTGCCCTGCGTTCGGGA
24	T10	62 TtGTGTtTGAGGCAGCGGACtTGATCATGCACACCCCGGGTGCGTGCCCTGCGTTCGGGA
10	D3	62 TcGTGTATGAGACAGCGGACATGATCATGCACACCCCGGGTGCGTGCCCTGCGTTCGGGA
9	D1	62 TtGTGTATGAGACAGCGGACATGATCATGCACACCCCGGGTGCGTGCCCTGCGTTCGGGA
14	HK5	62 TCGTGTAcGAGACAaCGGACATGATCATGCACACCCCTGGGTGCGTGCCCTGCGTTCGGGA
15	HK8	62 TCGTGTATGAaACAGCGGACATGATtATGCATACCCCTGGATGCaTGCCCTGCGTTCGGGA
12	HK3	62 TCGTGTATGAGACAGCaGACATGATCATGCATACCCCTGGATGCGTGCCCTGCGTaCGGGA
23	T3	62 TTGTGTATGAGACAGCGGACATGATCATGCACaACCCCTGGGTGCGTGCCCTGCGTTCGGGA
22	SW2	62 TTGTGTATGAGACAGCGGACATGATCATGCAtACCCCGGGTGCGTGCCCTGCGTTCGGGA
17	IND8	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACCCCGGGTGCGTGCCCTGCGTTCGGGA
16	IND5	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACtCCCGGGTGCGTGCCCTGCGTTCGGGA
21	SA10	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACCCCGGGTGCGTGCCCTGCGTTCGGGA
20	S45	62 TTGTGTATGAGGCAGtGGACgTGATCtTGACACCCCTGGGTGCGTGCCCTGCGTTCGGGA
25	US6	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACtCCCGGGTGCGTGCCCTGtGTTTCGGGA
13	HK4	62 TTGTGTATGAGGCAGCGGACATGATCATGCAtACCCCGGGTGCGTGCCCTGcGTcCGGGA
18	P10	62 TTGTGTATGAGGCAGCGGACATGATaATGCACACCCCGGGTGCGTGCCCTGtGTTTCGGGA
19	S9	62 TTGTGTAcGAGGCAGCGGACgTGATcATGCAtACCCCGGGTGtGTaCCCTGcGTTCaGGA
9-25	consensus	TtGTGTatGAggCAgcgGACaTGATcaTGCAcACcCCcGGgTGcgTgCCCTGcGTtCgGGA

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FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	123 GaaCAACcaCTCCCGtTGCTGGGTAGCGCTCACcCCCACGCTCGCGGCCAGGAACgCCAGC
24	T10	123 GGgCAACTCCTCCCGCTGCTGGGTAGCGCTCActCCCACGCTCGCGGCCAGGAACACCAGC
10	D3	123 GGACAACTCCTCTCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCGGCTAGGAATAGCAGC
9	D1	123 GGACAACTCCTCTCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCGGCTAGGAATGGCAaC
14	HK5	123 aaACAACTCCTCCCGTTGtTGGGTAGCGCTCgCCCCACGCTCGCGGCcAGGAACGcCAGC
15	HK8	123 GAACAACTCCTCCCGTTGcTGGGTgGCGCTCACTCCCACGCTCGCGGctAGGAATGTCAGC
12	HK3	123 GAACAACTCCTCCCGCTGtTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACGTCAGC
23	T3	123 GAgCAAtTCCTCCCGCTGCTGGGTAGCGCTtACTCCCACGCTCGCGGCCAGGAACGCCAGC
22	SW2	123 GGcCAACTCCTCCCGCTGCTGGGTAGCGCTCACTCCCACGCTaGCaGCCAGGAACaCCAGC
17	IND8	123 GGGCAACTtCTCTaGtTGCTGGGTAGCGCTCACTCCCCTCTCGCGGctAGGAACGCCAGC
16	IND5	123 GGGCAACTCCTCTCGCTGCTGGGTAGCGCTCACTCCCCTCTCGCGGCCAGGAACGCCAGC
21	SA10	123 GAACAACTCCTCCCGCTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAActCCAGC
20	S45	123 GAACAACTCCTCCCGtTGCTGGGTgGCGCTCACTCCCACGCTCGCGGCCAGGAActCCAGC
25	US6	123 GAACAAtTCCTCCCGcTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACGctAGC
13	HK4	123 GAACAACTCCTCCCGtTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACGCCAGC
18	P10	123 GAACAACTCCTCCCGcTGCTGGGTAGCGCTCACTCCCACaCTCGCGGctAGGAAttCCAGC
19	S9	123 GggtAACTCCTCCCaTGCTGGGTgGCGCTCACcCCCACgCTCGCGGCcAGGAACgCtAcc
9-25	consensus	gaacAActcCTCccgcTGcTGGGTaGCGCTcaCtCCCACgCTcGCgGCcAGGAACgcccAgC

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FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	184 aTCCCCACTACGACaATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
24	T10	184 GTCCCCACTACGACgATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
10	D3	184 GTCCCCACTACGACaATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
9	D1	184 GTCCCCACTACGGCgATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
14	HK5	184 GTCCCCACcACGGCAATACGACGCCACGTCGACTTGCTCGTTGGGGCGGCTGCTTTCTGCT
15	HK8	184 GTCCCCACtACGACAATACGACGCCACGTCGACTTGCTCGTTGGGGCGGCTGCTTTCTGCT
12	HK3	184 GTCCCCACcACGACAATACGACGTCACGTCGACTTGCTCGTTGGGGCGGCTGcTTCTGCT
23	T3	184 GTCCCCACTAaGACAATACGACGTCACGTCGACTTGCTCGTTGGGGCGGCTGCTTTCTGtT
22	SW2	184 GTCCCCACTACGACAATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGcT
17	IND8	184 GTCCCCACCACGACAATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGTT
16	IND5	184 GTCtCCACCACGACAATACGACaCCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGTT
21	SA10	184 GTCCCCACTACGACAATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
20	S45	184 GTCCCCACTACGACAATACGACGtCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
25	US6	184 GTCCCCACTACGACAATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTaCTTTCTGCT
13	HK4	184 aTCCCCACTACGACAATACGACGCCATGTCGAcTTGCTCGTTGGGGCGGCTGCTTTCTGCT
18	P10	184 GTCCCaACTACGgCAATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
19	S9	184 GTCCCcACcACGaCAATACGACGtCATGTCGATTGCTCGTTGGGGCGGCTGtTTTCTGCT
9-25	consensus	gTCCcCACTAcGaCaATACGACgcCAcGTCGAtTTGCTCGTTGGGGCGGCTgctTTCTGcT

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FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	245 CCGCTATGTAcGTGGGgGACCTCTGCGGATCcgTTTTCTCGTCTCTCAGCTGTTACCTT
24	T10	245 CCGCTATGTAtGTGGGaGACCTCTGCGGATCTGTTTTCTCGTCTCTCAGCTGTTACCTT
10	D3	245 CCGCCATGTACGTGGGGGATCTtTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTT
9	D1	245 CCGCCATGTACGTGGGGGATCTcTGCGGATCTGTTTTCTCaTCTCCAGCTGTTACCCcT
14	HK5	245 CCGCTATGTACGTGGGGGATCTtTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTT
15	HK8	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTT
12	HK3	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTT
23	T3	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTT
22	SW2	245 CCGtTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTT
17	IND8	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTT
16	IND5	245 CCGCTATGTACGTGGGGGATCTaTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTT
21	SA10	245 CCGCcATGTACGTGGGGGAcCTCTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTT
20	S45	245 CCGCTATGTACGTGGGGGATcCTCTGCGGATCTGTTTTCTCGTCTCCAGCTGTTACCTT
25	US6	245 CCGCTATGTACGTGGGGGAcCTCTGCGGgTCcTTTTCTCaTCTCCAGCTGTTACCTT
13	HK4	245 CCGCcATGTACGTGGGaGATCTCTGCGGATCTGTtTCCTCGTCTCCAGtTGTTACCTT
18	P10	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTtTCCTCGTCTCCAGCTGTTACCTT
19	S9	245 CCGCTATGTACGTGGGGGAcCTgTGCGGATCTGTTtTCCTCaTCTCCAGCTGTTACCaT
9-25	consensus	CCGctATGTACGTGGGgGAtCTcTGCGGaTCTGTtTCCTcgTcTCcCAGcTGTTACctT

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	306 tTCaCCTCGCCGGCATGAGACagcaCAGGACTGCAACTGCTCAATCTATCCCGGCCAcgTt
24	T10	306 CTCGCCTCGCCGGCATGAGACttTgCAGGACTGCAACTGCTCAATCTATCCCGGCCAtcTG
10	D3	306 CTCGCCTCGCCGGCATGAGACaGTACAGGAaTGTAAGTCTCAATCTATCCCGGCCACGTG
9	D1	306 CTCGCCTCGCCGGCATGAGACGGTACAGGAgtGTAAatTGCTCAATCTATCCCGGCCACGTG
14	HK5	306 CTCGCCTCGCCGACACGAGACGGTACAGGACTGCAACTGCTCAATCTATCCCGGCCACGTA
15	HK8	306 tTCGCCTCGCCGACACGAGACGGTACAGGACTGCAACTGCTCAATCTATCCCGGCCACGTA
12	HK3	306 CTCGCCTCGCCGACACGAGACAGTACAGGACTGCAACTGCTCAcTCTATCCCGGCCACGTA
23	T3	306 CTCGCCTCGCCGGCAtGAGACAGTACAGGACTGCAACTGCTCAATCTATCCCGGCCACGTA
22	SW2	306 tTCACCTCGCCGGCacGAGACAGTACAGGACTGCAACTGtTCCATCTATCCCGGCCACGTA
17	IND8	306 CTCACCGCGCCGGCATGAGACAGTACAGGACTGCAATTGCTCCATCTATCCCGGCCACGTA
16	IND5	306 CTCACCGCGCCGGCATGAGACAGTACAGGACTGCAATTGCTCCATCTATCCCGGCCACGTA
21	SA10	306 CTCGCCTCGCCGGtATGAGACAGTACAGGACTGCAATTGCTCAATCTATCCCGGCCgCGTA
20	S45	306 CTCGCCTCGTCGGCATGAGACAGTACAGGACTGCAAcTGTTCAATCTATCCCGGCCACGTA
25	US6	306 CTCGCCTCGTCaGCATGAGACAGTACAGGACTGCAATTGTTCAATCTATCCCGGCCACGTA
13	HK4	306 CTCGCCTCGCCGGCATGAGACgGTACAGGACTGCAATTGcTCAATCTATCCCGGCCACGTA
18	P10	306 CTCaCCTCGCCGGCATtgGACAGTACAGGACTGCAATTGtTCAATCTATCCtGGCCACGTA
19	S9	306 CTCgCCcCGtCGGCATgaGACAGTACAGaACTGCAATTGcTCAATCTATCCcGGaCACGTg
9-25	consensus	cTCgCCtCGcCggcAtgaGACagtaCAGgAcTGcAAcTGcTCaaTCTATCCcGGcCacgTa

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FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCaCCTACAACAGCcCTAGTGc
24	T10	367 TCAGGTCACCGCATGGCTTGGGAcATGATGATGAACTGGTCGCCTACAACAGCtCTAGTGG
10	D3	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCTACAgCAGCCCTAGTGG
9	D1	367 ACAGGTCACCGtATGGCTTGGGATATGATGATGAACTGGTCACCTACAACAGCCtTAGTGG
14	HK5	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAACAGCCCTAGTGG
15	HK8	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCgCCcACAACAGCCCTAGTGG
12	HK3	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCcCCTACAgCAGCCCTAGTGG
23	T3	367 aCAGGTCACCGtATGGCTTGGGATATGATGATGAACTGGTCgCCcACAaCgGCaCTAGTGG
22	SW2	367 TCAGGTCACCGCATGGCTTGGGAcATGATGATGAACTGGTCACCTACAGCaGCCCTgGTGG
17	IND8	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAGCgGCCCTAGTGG
16	IND5	367 TCAGGTCACCGCATGGCcTGGGATATGATGATGAACTGGTCACCTACAGCAGCCCTAGTGG
21	SA10	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAaCAGCtCTAGTaG
20	S45	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCgCCTACAGCAGCCtTAGTGG
25	US6	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAAtTGGTCACCTACAGCAGCCCTAGTGG
13	HK4	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAGCAGCCCTAGTGG
18	P10	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCcACAGCAGCCCTAGTGG
19	S9	367 aCAGGTCAtCGCATGGCcTGGGATATGATGATGAACTGGTCGCCtACAaCAGCCCTAGTGG
9-25	consensus	tCAGGTCaCCGcATGGCtTGGGATATGATGATGAACtGGTCaCCtACAgCaGCccTaGTgg

09084591.052696

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	428 TaTCGCAGTTACTCCGaATCCCACAAGCTGTCgTGGACATGGTGgCgGGGGCCCCACTGGGG
24	T10	428 TgTCGCAGTTACTCCGGATCCCACAAGCTGTCaTGGACATGGTGaCaGGGGCCCCACTGGGG
10	D3	428 TATCGCAGTTACTCCGGATCCCACAAGCTGTCgTGGACATGGTGgCGGGGGCCCCACTGGGG
9	D1	428 TATCGCAGTTACTCCGGATCCCACAAGCTGTCaTGGACATGGTGgCGGGGGCCCCACTGGGG
14	HK5	428 TGTCGCAGTTACTCCGGATCCCGCAAGCTGTCGTGGACATGGTaGCGGGGGCCCCACTGGGG
15	HK8	428 TGTCGCAGTTACTCCGGATCCCGCAAGCTaTCGTGGACATGGTGgCGGGGGCCCCACTGGGG
12	HK3	428 TGTCGCAaTTACTCCGGATCCCGCAAGCTGTCGTGGACATGGTGgCGGGGGCCCCACTGGGG
23	T3	428 TGTCGCAGTTgCTCCGGATCCCACAAGCTGTCGTGGACATGGTGgCGGGGGCCCCACTGGGG
22	SW2	428 TATCGCAGTTaCTCCGGATCCCACAAGCTGTCGTGGACATGGTaGCGGGGGCCCCACTGGGG
17	IND8	428 TATCGCAGTTGCTCCGGATCCCACAAGCTGTCGTGGATATGGTGgCGGGGGCCCCACTGGGG
16	IND5	428 TATCGCAGTTGCTCCGGATCCCACAAGCTGTCGTGGATATGGTGgCGGGGGCCCCACTGGGG
21	SA10	428 TATCGCAGTTACTCCGGATCCCACAAGCTaTCGTGGACATGGTGgCGGGGGCCCCACTGGGG
20	S45	428 TATCGCAGTTACTCCGGATCCCACAAGCTGTCGTGGACATGGTGgCGGGGGCCCCACTGGGG
25	US6	428 TATCGCAGTTACTCCGGATCCCACAAGCTGTCATGGACATGGTGgCGGGGGCCCCACTGGGG
13	HK4	428 TATCGCAGTTACTCCGaCTCCCACAAGCTGTCATGGACATGGTGgCGGGaGCCCCACTGGGG
18	P10	428 TgTCGCAGCTACTCCGGATCCCACAAGCTaTCtTGGATgTGGTGgCGGGGGCCCCACTGGGG
19	S9	428 TaTCGCAGCTACTCCGGATCCCACAAGCTgTCaTGGATaTGGTGgCGGGGGCCCCACTGGGG
9-25	consensus	TaTCGCAGtTaCTCCGgaTCCCaCAAGCTgTCgTGGAcATGGTgCgGGgGCCCCACTGGGG

D9084691.052698

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	489 AGTCCTGGCGGGCCTcGCCTACTAcTCCATGGCGGGGAAC TGGGCcAAGGTTTTAATTGTG
24	T10	489 AGTCCTGGCGGGCCTtGCCTACTATTCCATGGCGGGGAAC TGGGCTAAGGTTTTAATTGTG
10	D3	489 GGTCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTTTTGATTGTG
9	D1	489 GGTCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTTTTGATTGTG
14	HK5	489 GGTCTGGCGGGCCTTGCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTTTTGATTGTG
15	HK8	489 AGTCCTAGCGGGCCTTGCTACTATTCCATGGTGGGcAAC TGGGCTAAGGTTTTGATTGTG
12	HK3	489 AGTCCTAGCGGGCCTTGCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTTTTGATTGTG
23	T3	489 AGTCCTGGCGGGCCTTGCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTTTTGATTGTG
22	SW2	489 AGTCCTGGCGGGCCTTGCaTACTATTCCATGGTGGGGAAC TGGGCTAAGGTTTTGATTGTG
17	IND8	489 AATCCTGGCGGGCCTTGCTACTATTCCATGGTAGGGGAAC TGGGCTAAGGTTTTGATTGTG
16	IND5	489 AATCCTGGCGGGCCTTGCTACTATTCCATGGTAGGGGAAC TGGGCTAAGGTTTTGATTGTG
21	SA10	489 AGTCCTaGCGGGCCTTGCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTTTTGATTGTt
20	S45	489 AGTCCTGGCGGGCCTTGCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTTCTGATTGTG
25	US6	489 AGTCCTGGCGGGCCTTGCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTTCTGATTGTG
13	HK4	489 AGTCCTaGCGGGCCTTGctTACTATTCCATGGTGGGGAAC TGGGCcAAGGTTTTGATTGTG
18	P10	489 AGTCCTGGCGGGCCTTGCTACTATTCCATGGTGGGGAAC TGGGCTAAGGtTTGATTGTG
19	S9	489 AGTCCTGGCGGGCCTcGCCTACTATTCCATGGTGGGGAAC TGGGCTAAGGtTTGATTGTG
9-25	consensus	agTCCTgGCGGGCCTtGCcTACTAtTCCATGGtgGGgAAC TGGGctAAGGttTgATTGTg

09084691.052693

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	550 tTGCTACTCTTTGCCGGCGTTGATGGG 
24	T10	550 ATGCTACTCTTTGCCGGCGTTGATGGG 
10	D3	550 ATGCTACTCTTTGCTGGCGTcGACGGC 
9	D1	550 ATGCTACTCTTTGCTGGCGTTGACGGC 
14	HK5	550 ATGCTACTtTTTGCCGGCGTTGATGGG 
15	HK8	550 ATGCTACTgTTTGCCGGCGTTGATGGG 
12	HK3	550 ATGCTACTtTTTGCCGGCGTTGATGGG 
23	T3	550 cTGCTACTCTTTGCCGGCGTTGATGGG 
22	SW2	550 ATGCTACTCTTTGCTGGCGTTGACGGG 
17	IND8	550 ATGCTACTCTTTGCCGGCGTTGACGGG 
16	IND5	550 ATGCTACTCTTTGCCGGCGTTGACGGG 
21	SA10	550 ATGCTACTCTTTGCCGGCGTTGACGGG 
20	S45	550 ATGCTACTCTTTGCCGGCGTTGACGGG 
25	US6	550 tTGCTACTCTTTGCCGGCGTTGACGGG 
13	HK4	550 ATGCTACTCTTTGCCGGCGTTGACGGG 
18	P10	550 ATGCTACTCTTTGCCGGCGTTGACGGa 
19	S9	550 ATGCTACTtTTTGCTGGtGTTGACGGg 
9-25	consensus	aTGCTACTcTTTGCCcGGcGTtGAcGGg

09084591.052598

FIGURE 1C

SEQ ID NO:	Isolate
26	T2
27	T4
28	T9
29	US10
26-29	consensus

1 GCcCAAGTGAGGAACACCAGccgCgGtTACATGGTGACTAACGACTGTTCCaATGAgAGC  
 1 GCaCAAGTGAAGAACACCACtAaCAGCTACATGGTGACCcAACGACTGTTctAATGACAGCA  
 1 GCCgAAGTGAAGAACACCAGTACCAGCTACATGGTGACaAATGACTGTTCCAACGACAGCA  
 1 GtCcAAGTGAAaAACACCAGTACCAGCTAtATGGTGACCcAATGACTGcTCCAACGACAGCA  
 GcccAAGTGAagAACACCAGtAcCaGcTAcATGGTGACCcAA-GACTGtTCCAA-GAcAGCA

SEQ ID NO:	Isolate
26	T2
27	T4
28	T9
29	US10
26-29	consensus

62 TCACcTGGCAGCTCCaAGCCGCGGTtCTCCACGTCCCCGGGTGTaTCCCGTGtGAGAggct  
 62 TCACtTGGCAGCTCCAGGCCGCGGTCTCCACGTCCCCGGGTGTGTCCCGTGCGAGAAaAc  
 62 TCACcTGGCAACTCCAGGCCGCGGTCTCCACGTCCCCGGGTGcGTCCCGTGCGAGAgAGT  
 62 TCACtTGGCAACTtgAGGCTGCGGTCTCCACGTtCCCCGGGTGtGTCCCGTGCGAGAAAGT  
 TCAC-TGGCA-CTccAgGCcGCGGTcCTCCACGTcCCCCGGGTGtgTCCCGTGcGAGA-agt

SEQ ID NO:	Isolate
26	T2
27	T4
28	T9
29	US10
26-29	consensus

123 GGGAAATACATCcCGaTGCTGGATACCGGTcaCACCAAACGTGGCCGTGCGGCAGCCCGGC  
 123 GGGAAATACATCtCGGTGCTGGATACCGGTtTCACCAAACGTGGCCGTGCGGCAGCCCGGC  
 123 tGGAAAcgCgTCgCGGTGCTGGATACCGGTCTCgCCAAACGTaGcTGTGCAGCGGCCTGGC  
 123 gGGAAAtaCaTCtCGGTGCTGGATACCGGTCTCaCCAAAtGTgGCcGTGCAGCGGCCTGGC  
 gGGAAAtaCaTCtCGgTGCTGGATACCGGTctCaCCAAAcGTgGCcGTGC-GC-GCC-GGC

SEQ ID NO:	Isolate
26	T2
27	T4
28	T9
29	US10
26-29	consensus

184 GCtCTtACGCAGGGCTTGCGGACGCACATcGACATGGTTGTGATGTCCGCCACGCTCTGCT  
 184 GCCCTCACGCAGGGCTTGCGGACGCACATtGACATGGTTGTGATGTCCGCCACGCTCTGCT  
 184 GCCCTCACGCAGGGCTTGCGGACGCACATCGACATGGTTGTGATGTCCGCCACGCTCTGCT  
 184 GCCCTCACGCAGGGCTTGCGGACtCACATCGACATGGTcGTGATGTCCGCCACGCTCTGCT  
 GCcCTcACGCAGGGCTTGCGGACgCACATcGACATGGTtGTGATGTCCGCCACGCTCTGCT

SEQ ID NO:	Isolate
26	T2
27	T4
28	T9
29	US10
26-29	consensus

245 CTGCcCTcTACGTGGGGGACCTCTGCGGCGGGGTGATGCTCGCAGCCCAGATGTTcATtGT  
 245 CTGCTCTtTACGTGGGGGACCTCTGCGGCGGGGTGATGCTCGCAGCCCAGATGTTcATcGT  
 245 CCGCTCTcTACGTGGGGGAtCTCTGCGGCGGGGTaATGCTCGCcGCtCAGATGTTcATTaT  
 245 CCGCTCTtTACGTGGGGGActTCTGCGGtGGGaTgATGCTCGCaGCCcCAaATGTTcATTgT  
 C-GCtCT-TACGTGGGGGAccTCTGCGGcGGGgTgATGCTCGCaGCCcCAgATGTTcATTgT

	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---

[illegible][illegible]

84892\_1



FIGURE 1D

SEQ ID NO:    Isolate

33                    T8

30                    DK8

32                    SW3

31                    DK11

30-33                consensus

1 GTGGAAGTtAGaAACAcCAGTTtTAGCTACTACGCCACCAATGATTGCTCgAACAAACAGCA  
 1 GTGGAAGTCAGGAACATCAGTTcAGCTACTACGCCACCAATGATTGCTCAAACAACAGCA  
 1 GTGGAAGTCAGGAACATCAGTTCTAGCTACTAtGCCACCAATGATTGCTCAAACAgCAGCA  
 1 GTGGAAGTCAGGAACAcCAGTTCTAGtTACTAcGCCACCAATGATTGCTCAAACAaCAGCA  
 GTGGAAGTcAGgAACa - CAGTTtAGcTACTAcGCCACCAATGATTGCTCaAACAAcCAGCA

SEQ ID NO:    Isolate

33                    T8

30                    DK8

32                    SW3

31                    DK11

30-33                consensus

62 TCACCTGGCAgCTCACCaaCGCAGTTCTCCACCTTCCCGGATGCGTCCCATGTGAGAATGA  
 62 TCACCTGGCAACTCACCgACGCAGTTCTCCACCTTCCCGGATGCGTCCCATGTGAGAATGA  
 62 TCACCTGGCAACTCACCaaCGCAGTcCTCCACCTTCCCGGATGCGTCCCGTGTGAGAATGA  
 62 TCACCTGGCAACTCACCaaCGCAGTtCTCCACCTTCCCGGATGCGTCCCaTGTGAGAATGA  
 TCACCTGGCAaCTCACCaaCGCAGTtCTCCACCTTCCCGGATGCGTCCCaTGTGAGAATGA

SEQ ID NO:    Isolate

33                    T8

30                    DK8

32                    SW3

31                    DK11

30-33                consensus

123 CAATGGCACCTtTGCGCTGCTGGATACAAGTaACACCTAATGTGGCTGTGAAACACCGtGGC  
 123 CAATGGCACCTTGCGCTGCTGGATACAAGTGACACCTAATGTGGCTGTGAAACACCGCGGC  
 123 tAATGGCACCTTGCACTGCTGGATACAAGTGACACCTAATGTGGCTGTGAAACACCGCGGC  
 123 cAATGGCACCTTGCACTGCTGGATACAAGTGACACCTAATGTGGCTGTGAAACACCGCGGC  
 cAATGGCACCTtGc - CTGCTGGATACAAGTgACACCTAATGTGGCTGTGAAACACCGcGGC

SEQ ID NO:    Isolate

33                    T8

30                    DK8

32                    SW3

31                    DK11

30-33                consensus

184 GCACTcACTCAcAACCTGCGAACgCatGTCGACGTGATCGTAATGGCAGCTACGGTCTGCT  
 184 GCACTtACTCAtAACCTGCGAACACACGTGCGACGTGATCGTAATGGCAGCTACGGTCTGCT  
 184 GCgCTCACTCACAACCTGCGAGCACACGTGATATGATCGTAATGGCAGCTACGGTCTGCT  
 184 GCaCTCACTCACAACCTGCGAGCACAtaTaGATATGATtGTAATGGCAGCTACGGTCTGCT  
 GCaCTcACTCAcAACCTGCGA - CaCA - gTcGA - - TGATcGTAATGGCAGCTACGGTCTGCT

SEQ ID NO:    Isolate

33                    T8

30                    DK8

32                    SW3

31                    DK11

30-33                consensus

245 CGGCCTTGATGTGGGgGACGTgTGCGGGGCCGTGATGATaGcGTCGAGGCTtTCATAAT  
 245 CGGCCTTGATGTGGGAGACGTaTGCGGGGCCGTGATGATCGTGTCGAGGCTtTCATAAT  
 245 CGGCCTTGATGTGGGAGACaTGTCGGGGCCGTGATGATCGTGTCGAGGCTTTTCATAAT  
 245 CGGCCTTGATGTGGGAGACgTGTCGGGGCCGTGATGATCGTGTCGAGGCTTTTCATAgT  
 CGGCCTTGATGTGGGaGACgTgTGCGGGGCCGTGATGATcGtGTCGAGGCTtTCATAaT

FIGURE 1D

SEQ ID NO:    Isolate

33                    T8

30                    DK8

32                    SW3

31                    DK11

30-33                consensus

306 ATCGCCaGAACGCCACAACCTTcACCCAGGAGTGCAACTGTTCCATCTACCAAGGTCATATC  
 |||||  
 306 ATCGCCtGAACGCCACAACCTTTACCCAGGAGTGCAACTGTTCCATCTACCAAGGTCATATC  
 |||||  
 306 ATCGCCAGAACGCCACAACCTTTACCCAAGAGTGCAACTGTTCCATCTACCAAGGTCgTATC  
 |||||  
 306 ATCGCCAGAAcCaCCaCaCTTTACCCAAGAGTGCAACTGTTCCATCTACCAAGGTCacATC  
 |||||  
 ATCGCCaGAACgCCACaACTTtACCCA-GAGTGCAACTGTTCCATCTACCAAGGTCatATC

SEQ ID NO:    Isolate

33                    T8

30                    DK8

32                    SW3

31                    DK11

30-33                consensus

367 ACCGGCCACCGCATGGCATGGGACATGATGCTgAACTGGTCACCAACTCTcACCATGATCC  
 |||||  
 367 ACCGGCCACCGCATGGCATGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC  
 |||||  
 367 ACCGGCCACCGCATGGCgTGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC  
 |||||  
 367 ACCGGCCACCGCATGGCaTGGGACATGATGCTtAACTGGTCACCAACTCTcACCATGATCC  
 |||||  
 ACCGGCCACCGCATGGCaTGGGACATGATGCTaAACTGGTCACCAACTCT-ACCATGATCC

SEQ ID NO:    Isolate

33                    T8

30                    DK8

32                    SW3

31                    DK11

30-33                consensus

428 TCGCCTAcGcTcGCTCGTGTgCCTGAaCTAGtCCTtgAaGTTGTCTTCGGCGGCCATTGGGG  
 |||||  
 428 TCGCCTATGCCGCTCGTGTTCCTGAGCTAGcCCTccAgGTTGTCTTCGGCGGCCATTGGGG  
 |||||  
 428 TtGCCTATGCCGCTCGTGTTCCTGAGCTAGTCCTTGAAGTTGTCTTCGGCGGCCATTGGGG  
 |||||  
 428 TcGCCTATGCCGCcCGTGTTCCTGAGCTAGTCCTTGAAGTcGTCTTCGGtGGtCATTGGGG  
 |||||  
 TcGCCTAtGCcGcTcCGTGTtCCTGAgCTAGtCCTtgAaGtGTCTTCGGcGGcCATTGGGG

SEQ ID NO:    Isolate

33                    T8

30                    DK8

32                    SW3

31                    DK11

30-33                consensus

489 CGTGGTGTTTGGCTTGGCCTATTTCTCCATGCAaGGAGCGTGGGCCAAAGTCATcGCCATC  
 |||||  
 489 CGTGGTGTTTGGCTTGGCCTATTTCTCCATGCAGGGAGCGTGGGCCAAAGTCATTGCCATC  
 |||||  
 489 CGTGGTGTTTGGCTTGGCCTATTTCTCCATGCAaGGAGCGTGGGCCAAAGGTCATTGCCATC  
 |||||  
 489 tGTGGTGTTTGGCTTGGCCTATTTCTCCATGCAGGGAGCGTGGGCCAAAGGTCATTGCCATC  
 |||||  
 cGTGGTGTTTGGCTTGGCCTATTTCTCCATGCA-GGAGCGTGGGCCAA-GTCATtGCCATC

SEQ ID NO:    Isolate

33                    T8

30                    DK8

32                    SW3

31                    DK11

30-33                consensus

550 CTCCTcCTTGTCGCAGGAGTGGAcGCA  
 |||||  
 550 CTCCTtCTTGTCGCAGGAGTGGATGCA  
 |||||  
 550 CTCCTgCTTGTCGCAGGAGTGGATGCA  
 |||||  
 550 CTCCTtCTTGTAcGCAGGAGTGGATGCA  
 |||||  
 CTCCTtCTTGTCGCAGGAGTGGATGCA

FIGURE 1B

SEQ ID NO: Isolate  
35 DK12

36 HK10

37 S2

39 S54

38 S52

35-39 consensus

1 tTAGAGTGGCGGAATGTGTCCGGCCTCTAcGTCCTTACCAACGACTGTtCCAATAGCAGTA  
1 CTAGAGTGGCGGAATGTGTCTGGCCTCTATGTCCTTACCAACGACTGTtCCAATAGCAGTA  
1 CTAGAGTGGCGGAATACGTCTGGCCTCTATGTCCTtACCAACGACTGTTCCAATAGCAGTA  
1 CTAGAGTGGCGGAATACGTCTGGCCTCTATaTCCTTACCAACGACTGTTCCAATAGCAGTA  
1 CTAGAGTGGCGGAATACGTCTGGCCTCTATgTCCTTACCAACGACTGTTCCAATAGCAGTA  
cTAGAGTGGCGGAATAcGTCtGGCCTCTAtgTCCTtACCAACGACTGTtCCAATAGCAGTA

SEQ ID NO: Isolate  
35 DK12

36 HK10

37 S2

39 S54

38 S52

35-39 consensus

62 TcGTGTATGAGGCCGATGACGTCATTCTGCACACACCTGGCTGTGTACCTTGTGTTcAGGA  
62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACACCTGGCTGTGTACCTTGTGTTcAGGA  
62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACACCTGGCTGTGTACCTTGTGTTcAGGA  
62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACACCCGGCTGTGTACCTTGTGTTcAGGA  
62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACACCCGGCTGTGTACCTTGTGTTcAGGA  
TtGTGTATGAGGCCGATGACGTCATTCTGCACACACCTGGCTGTGTACCTTGTGTTcAGGA

SEQ ID NO: Isolate  
35 DK12

36 HK10

37 S2

39 S54

38 S52

35-39 consensus

123 CGGCAATACATCtACGTGCTGGACCTCaGTGACgCCTACAGTGGCAGTCAGGTACGTCGGA  
123 CGGCAATACATCCACGTGCTGGACCTCgGTGACACCTACAGTGGCAGTCAGGTACGTCGGA  
123 CGGtAATACATCCACGTGCTGGACCCcAGTGACACCTACAGTGGCAGTCAGGTAtGTCGGA  
123 CGGCAATACATCCACGTGCTGGACCCcAGTGACACCTACGGTGGCAGTCAGGTACGTCGGA  
123 CGGCAATACATCCAtGTGCTGGACCCcAGTGACACCTACGGTGGCAGTCAGGTACGTCGGA  
CGGcAATACATCCAcGTGCTGGACCCcCaGTGACaCCTACaGTGGCAGTCAGGTACGTCGGA

SEQ ID NO: Isolate  
35 DK12

36 HK10

37 S2

39 S54

38 S52

35-39 consensus

184 GCAACCACCGCtTCGATACGCAGTCATGTGGACCTGcTAGTGGGCGCGGCCACGATGTGCT  
184 GCAACCACCGCcTCGATACGCAGTCATGTGGACCTGTTAGTGGGCGCGGCCACGATGTGCT  
184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTATTgGTGGGCGCGGCCACtATGTGCT  
184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTATTAGTGGGCGCGGCCACGCTGTGCT  
184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTATTAGTGGGCGCGGCCACGCTGTGCT  
GCAACCACCGCtTCGATACGCAGTCATGTGGACCTAtTaGTGGGCGCGGCCACgaTGTGCT

FIGURE 1E

SEQ ID NO: Isolate

35 DK12  
36 HK10  
37 S2  
39 S54  
38 S52  
35-39 consensus

245 CTGCGCTCTACGTGGGtGATgTGTGTGGGGCCGTCTTCCTtGTGGGACAAGCCTTCACGTT  
245 CTGCGCTCTACGTGGGcGATATGTGTGGGGCCGTCTTCCTCGTGGGACAAGCCTTCACGTT  
245 CTGCGCTCTACGTGGGTGATATGTGTGGGGCCGTCTTTCTCGTGGGACAAGCCTTCACGTT  
245 CTGCGCTCTATGTGGGTGATATGTGTGGGGCCGTCTTTCTCGTGGGACAAGCCTTCACGTT  
245 CTGCGCTCTATGTGGGTGATATGTGTGGGGCCGTCTTTCTCGTGGGACAAGCCTTCACGTT  
CTGCGCTCTAcGTGGGtGATaTGTGTGGGGCCGTCTTtCTcGTGGGACAAGCCTTCACGTT

SEQ ID NO: Isolate

35 DK12  
36 HK10  
37 S2  
39 S54  
38 S52  
35-39 consensus

306 CAGACcTCGTGCGCCATCAAACaGTCCAGACCTGTAACtGCTCGCTGTACCCAGGCCAtCTT  
306 CAGACcTCGTGCGCCATCAAACGGTCCAGACCTGTAACtGCTCGCTGTACCCAGGCCAcCTT  
306 CAGACCTCGTCGCGCCATCAAACGGTCCAGACCTGTAACtGCTCGCTGTACCCAGGCCATCTT  
306 CAGACCTCGTCGCGCCATCAAACGGTCCAGACCTGTAACtGCTCGCTGTACCCAGGCCATCTT  
306 CAGACCTCGTCGCGCCATCAAACGGTCCAGACCTGTAACtGCTCGCTGTACCCAGGCCATgTT  
CAGACcTCGTGCGCCATCAAACgGTCCAGACCTGTAACtGCTCGCTGTACCCAGGCCAtcTT

SEQ ID NO: Isolate

35 DK12  
36 HK10  
37 S2  
39 S54  
38 S52  
35-39 consensus

367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGctGTGGGTATGGTGG  
367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCcGTGGGTATGGTGG  
367 TCAGGACATCGcATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG  
367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG  
367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG  
TCAGGACATCGaATGGCTTGGGATATGATGATGAATTGGTCCCCCGctGTGGGTATGGTGG

SEQ ID NO: Isolate

35 DK12  
36 HK10  
37 S2  
39 S54  
38 S52  
35-39 consensus

428 TaGCGCACGTCTGCGtTGCCCCAGACCTTGTTTCGACATAATAGctGGGGCCCATTTGGGG  
428 TGGCGCACGTCTGCGgTGCCCCAGACCTTGTTTCGACATAATAGCCGGGGCCCATTTGGGG  
428 TGGCGCACGTtCTGCGtTGCCCCAGACcTGTTTCGACATAATAGCCGGGGCCCATTTGGGG  
428 TGGCGCACATCCTGCGATTGCCCCAGACCTTGTTTTCGACATACTGGCCGGGGCCCATTTGGGG  
428 TGGCGCACATCCTGCGATTGCCCCAGACCTTGTTTTCGACATACTGGCCGGGGCCCATTTGGGG  
TgGCGCACgTcCTGCG- tTGCCCCAGACCTTGTTTCGACATAaTaGccGGGGCCCATTTGGGG

FIGURE 1E

<u>SEQ ID NO:</u>	<u>Isolate</u>
35	DK12
36	HK10
37	S2
39	S54
38	S52
35-39	consensus

```

489 CATCaTGGCgGGCCTAGCCTATTACTCCATGCAGGGCAACTGGGCCAAGGTCGCTATCATC
|||
489 CATCTTGGCaGGCCTAGCCTATTACTCCATGCAGGGCAACTGGGCCAAGGTCGCTATCATC
|||
489 CATCTTGGCGGGCCTAGCCTATTACTCCATGCAaGGCAACTGGGCCAAGGTCGCTATCATC
|||
489 CATCTTGGCGGGCCTAGCCTATTATTCTATGCAGGGCAACTGGGCCAAGGTCGCTATCATC
|||
489 CATCTTGGCGGGCCTAGCCTATTATTCTATGCAGGGCAACTGGGCCAAGGTCGCTATtgTC
|||
CATCtTGGCgGGCCTAGCCTATTAcTCaATGCagGGCAACTGGGCCAAGGTCGCTATcaTC

```

<u>SEQ ID NO:</u>	<u>Isolate</u>
35	DK12
36	HK10
37	S2
39	S54
38	S52
35-39	consensus

```

550 ATGGTTATGTTTTTCAGGaGTCGATGCC
|||
550 ATGGTTATGTTTTTCAGGGGTCGATGCC
|||
550 ATGGTTATGTTTTTCAGGGGTCGAcGCC
|||
550 ATGATTATGTTTTTCAGGGGTCGATGCC
|||
550 ATGATTATGTTTTTCAGGGGTCGATGCC
|||
ATGgTTATGTTTTTCAGGgGTCGAtGCC

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00041691.052699

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43 27

42 Z6

1 GTcAACTATCaCAATGCCTCGGGCGTCTATCACATCACCAACGACTGCCGAACTCGAGCA  
 |||  
 1 GTtAACTATCGCAATGCCTCGGGCGTCTATCACGTACCAACGACTGCCGAACTCGAGCA  
 |||  
 GTtAACTATCgCAATGCCTCGGGCGTCTATCACgTCACCAACGACTGCCGAACTCGAGCA

43 27

42 26

62 TAA TGTATGAGGCCGAACACCACATCCTACACCTCCCAGGGGTGCGTACCCTGTGTGAGGGa  
62 TAGTGTATGAGGCCGAACACCAgATCTTACACCTCCCAGGGGTGcTgCCCTGTGTGAGGGt  
TagTGTATGAGGCCGAACACCAgATCtTACACCTCCCAGGGGTGcTgCCCTGTGTGAGGGt

43 27

42 26

123 gGGGAACCAAGTCACGCTGCTGGGTGGCCCTTACTCCCACCGTGGCGGcGcCTTATATCGGT  
123 tGGGAAtCAGTCACGCTGCTGGGTGGCCCTTACTCCCACCGTGGCGGtGtCTTATATCGGT  
tGGGAAtCAGTCACGCTGCTGGGTGGCCCTTACTCCCACCGTGGCGGtGtCTTATATCGGT

43 27

42 26

184 GCaCCGCTTGAaTCCaTCCGGAGACATGTGGACCTGATGGTAGGCGCtGCTACaGTGTGCT  
184 GCTCCGCTTGAcTCCcTCCGGAGACATGTGGACCTGATGGTGGGCGCCGCTACTGTaTGCT  
GCTCCGCTTGAcTCCcTCCGGAGACATGTGGACCTGATGGTgGGGCGCcGCTACtGTaTGCT

13 27

12 26

245 CcGcTcCTCTACaTTGGGGACCTGTGCGGTGGcGtATTtTTGGTTGGtCAGATGTTtTCCTTT  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
245 CtGCCCTCTACgTTGGAGAtCTGTGCGGTGGTGcATTCTTGGTTGGcCAGATGTTCTCCTT  
  
CtGCCCTCTACgTTGGaGAtCTGTGCGGTGGtGcATTCTTGGTTGGcCAGATGTTcTCcTT

**13** **27**

26

306 CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCCATCTATGCgGGGCacgTt  
 306 CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCTATCTACGCAGGGCATATC  
 CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCTATCTACGCaGGGCataTc

3                      27

2 26

367 ACaGGCCACAGaATGGCATGGGACATGATGATGAACTGGAGTCCCACAACCACCTtTGgTCC  
 |||||  
 367 ACgGGCCACAGgATGGCATGGGACATGATGATGAACTGGAGTCCCACAACCACCTGcTtC  
 |||||  
 ACgGGCCACAGgATGGCATGGGACATGATGATGAACTGGAGTCCCACAACCACCTgTgTtC

FIGURE 1F

SEQ ID NO:    Isolate  
 43                    Z7  
 42                    Z6  
 42-43 consensus (Z6)

428 TCGCCCAGGTtATGAGGATCCCTAGCACTCTGGTgGACCTACTCaCTGGAGGGCACTGGG  
 |||||  
 428 TCGCCCAGGTcATGAGGATCCCTAGCACTCTGGTaGAtCTACTCGCTGGAGGGCACTGGG  
 TCGCCCAGGTcATGAGGATCCCTAGCACTCTGGTaGAtCTACTCgCTGGAGGGCACTGGG

SEQ ID NO:    Isolate  
 43                    Z7  
 42                    Z6  
 42-43 consensus (Z6)

489 taTCCTTaTcGGGgTGGCaTACTTcTGCATGCAAGCTAATTGGGCCAAGGTCATtCTGGTC  
 |||||  
 489 CgTCCTTGTTGGGtTGGCGTACTTCAGtATGCAAGCTAATTGGGCCAAaGTCATCCTGGTC  
 cgTCCTTgTtGGGtTGGCgTACTTCaGtATGCAAGCTAATTGGGCCAAaGTCATcCTGGTC

SEQ ID NO:    Isolate  
 43                    Z7  
 42                    Z6  
 42-43 consensus (Z6)

550 CTTTTCTCTaCGCTGGAGTTGATGCC  
 |||||  
 550 CTTTTCTCTtCGCTGGAGTTGATGCC  
 CTTTTCTCTtCGCTGGAGTTGATGCC

09084691.052698

FIGURE 1G

SEQ ID NO: Isolate

45 SA1  
47 SA5  
49 SA7  
46 SA4  
50 SA13  
48 SA6  
45-50 consensus

1 GTtCCCTACCGgAATGCCTCTGGGGTTTAcCATGTCACCAATGAcTGCCCAAACTCcTCCA  
1 GTCCCCTACCGAAATGCCTCTGGGGTTTATCATGTCACCAATGATTGCCCAAACTCTTCCA  
1 GTCCCCTACCGAAATGCCTCcGGGGTTTATCATGTCACCAATGATTGCCCGAACTCTTCCA  
1 GTTCCCTACCGAAAcGCCTCTGGGGTTTATCATGTCACCAATGATTGCCCAAACTCTTCCA  
1 GTTCCCTACCGAAATGCCTCTGGGGTTTATCATGTCACCAATGATTGCCCAAACTCTTCCA  
1 GTTCCtTACCGgAATGCCTCTGGGGTgTATCATGTtACCAATGATTGCCCAAACTCTTCCA  
GTtCCcTACCGaAAtGCCTCtGGGGTtTAtCATGTcACCAATGAtTGCCCaAACTCtTCCA

SEQ ID NO: Isolate

45 SA1  
47 SA5  
49 SA7  
46 SA4  
50 SA13  
48 SA6  
45-50 consensus

62 TAGTCTACGAGGCTGATAgCCTGATctTGCACGCACCTGGcTGCCTGCCCTGTGTCAgGcA  
62 TAGTCTACGAGGCTGATAACCTGATtCTGCACGCACCTGGTTGCGTGCCCTGTGTCAaGgA  
62 TAGTCTAtGAGGCTGAcAACCTGATCCTGCACGCACCTGGTTGCGTGCCCTGTGTCAgAcA  
62 TAGTtTACGAGGCTGATAACCTGATCTTGCAtGCACCTGGTTGCGTGCCtTGTGTcAGGCA  
62 TcGTCTACGAGGCTGATGACCTGATCTTACACGCACCTGGTTGCGTGCCCTGTGTtAGGCA  
62 TaGTCTAtGAGGCTGATGACCTGATCcTACACGCACCTGGcTGCCTGCCCTGTGTccGGaA  
TaGTcTAcGAGGCTGAtaaCCTGATc-TgCAcGCACCTGGtTGCCTGCCcTGTGTcaggcA

SEQ ID NO: Isolate

45 SA1  
47 SA5  
49 SA7  
46 SA4  
50 SA13  
48 SA6  
45-50 consensus

123 AGaTAATGTCAGTAGGTGCTGGGTCCAAATCACCCCCACAcTGTCAGCCCCGAcCtTCGGA  
123 AGgTAATGTCAGTAGGTGCTGGGTCCAAATCACCCCCACATTGTcAGCCCCGAACCTCGGA  
123 AaATAATGTCAGTAGGTGCTGGGTCCAAATCACCCCCACATTGTcAGCCCCGAACCTCGGA  
123 AGATAATGTCAGTAaGTGCTGGGTCCAAATCACCCCCACgTTGTcAGCCCCGAAtCTCGGA  
123 GGgTAATGTCAGTAGGTGCTGGGTCCAgATCACCCCCACACTGTcAGCCCCGAGCCTCGGA  
123 GGaTAATGTCAGTAGaTGCTGGGTtCatATCACCCCCACACTaTCAGCCCCGAGCCTCGGA  
agaTAATGTCAGTAggTGCTGGGTcCaaATCACCCCCACa-TgTCAGCCCCGAaccTCGGA



FIGURE 1G

<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	184 GCGGTCACGGCTCCTCTTCGGAGGGcCGTTGACTACTTAGCGGGAGGaGCTGctCTCTGcT
47	SA5	184 GCGGTCACGGCTCCTCTTCGGAGGGtCGTTGACTACTTAGCGGGAGGGGCTGCCCTCTGcT
49	SA7	184 GCGGTCACGGCTCCTCTTCGGAGGGCCGTTGACTACcTAGCGGGAGGGGCTGCCCTCTGcT
46	SA4	184 GCGGTCACGGCTCCTCTTCGGAGGGCCGTTGACTACTTAGCGGGAGGGGCTGCCCTCTGcT
50	SA13	184 GCGGTCACGGCTCCTCTTCGGAGGGCCGTTGACTACTTAGCGGGgGGGGCTGCCCTtTGcT
48	SA6	184 GCGGTCACGGCTCCTCTTCGGAGGGCCGTTGAtTACTTgGCGGGaGGGGCcGCCCTgTGCT
45-50	consensus	GCGGTCACGGCTCCTCTTCGGAGGGcCGTTGAcTAcTaGCGGGaGGgGcTGCcTcTGCT
<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	245 CCGCACTATACGTCGGcGACGCGTGCGGGGCAGTGTTtcTGGTAGGCCAAATGTTcACCTA
47	SA5	245 CCGCACTATACGTCGGGGACGCGTGCGGGGCAGTGTTcTTGGTAGGCCAAATGTTcACCTA
49	SA7	245 CCGCgCTATACGTCGGGGACGCGTGCGGGGCAGTGTTTTTGGTAGGCCAgATGTTcAgCTA
46	SA4	245 CCGCaCTATACGTCGGGGACGCGTGCGGGGCAGTGTTTTTGGTAGGCCAAATGTTcACCTA
50	SA13	245 CCGCGTTATACGTCGGAGACGCGTGCGGGGCAGTGTTTTTGGTAGGtCAAATGTTcACCTA
48	SA6	245 CCGCGTTATACGTCGGAGACGtGTGCGGGGCAtTGTTTTTGGTAGGcCAAATGTTcACCTA
45-50	consensus	CCGC - cTATACGTCGGgGACGcGTGCGGGGCAGTGTTtcTGGTAGGcCaAATGTTcAcCTA
<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	306 TAGGCCTCGCCAGCATAcAcAGTGcAGGACTGCAACTGTTCCATTtTACAGtGGCCATATC
47	SA5	306 TAGGCCTCGCCAGCATAcTACGGTGcAGGACTGCAACTGTTCCATTtTACAGcGGCCATATC
49	SA7	306 TAGGCCTCGCCAGCACACTACGGTGcAGGACTGCAACTGTTCCATTtTACAGTGGCCATATC
46	SA4	306 TAGGCCTCGCCAGCACACTACGGTGCAaGACTGCAATtGcTCtATTtTACAGTGGCCATATC
50	SA13	306 TAGcCCTCGCCgGCATAaTgttGTGcAGGACTGCAACTGtTCCATTtTACAGTGGCCAcATC
48	SA6	306 TAGgCCTCGCCaGCATgcTacgGTaCAGGACTGCAACTGcTCCATTtTACAGTGGCCAtATC
45-50	consensus	TAGgCCTCGCCaGCAtactacgGTgCAGGACTGCAAcTgTTCcATTtTACAGtGGCCAtATC
<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	367 ACCGGCCACCGgATGGCtTGGGACATGATGATGAATTGGTCACCTACGACAGCCTTGcTGA
47	SA5	367 ACCGGCCACCGAATGGCATGGGACATGATGATGAATTGGTCACCTACGACAGCCTTGGTGA
49	SA7	367 ACCGGCCACCGAATGGCATGGGACATGATGATGAATTGGTCACCTACGACAGCCTTGGTGA
46	SA4	367 ACCGGCCACCGGATGGCATGGGACATGATGATGAATTGGTCACCTACGACgGCCTTGcTGA
50	SA13	367 ACCGGCCACCGGATGGCATGGGACATGATGATGAATTGGTCACCTACaACAGCtTTGGTGA
48	SA6	367 ACTGGCCACCGGATGGCATGGGACATGATGATGAATTGGTCACCcgCgACAGCtTTGGTGA
45-50	consensus	ACcGGCCACCGgATGGCaTGGGACATGATGATGAATTGGTCACCTaCgACaGCcTTGgTGA

FIGURE 1G

<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	428 TGGCCCAGaTGCTACGGATcCCCCAgGTGGTCATaGACATCATaGCCGGGGGCCACTGGGG
47	SA5	428 TGGCCCAGgTGCTACGGATTCCCCAaGTGGTCATtGACATCATTGCCGGGGGCCACTGGGG
49	SA7	428 TGGCCCAGTTGCTACGGATTCCCCAGGTGGTCATCGACATCATTGCCGGGGGCCACTGGGG
46	SA4	428 TGGCCCAGTTGCTACGGATTCCCCAGGTGGTCATCGACATCATTGCCGGGGGCCACTGGGG
50	SA13	428 TGGCCCAGTTGtTACGGATTCCCCAGGTGGTCATTGACATCATTGCCGGGGcCCACTGGGG
48	SA6	428 TGGCCCaaTGcTACGGATTCCCCAGGTGGTCATTGACATCATTGCCGGGGgCCACTGGGG
45-50	consensus	TGGCCCAGtTGcTACGGATtCCCCAgGTGGTCATtGACATCATtGCCGGGGgCCACTGGGG

<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	489 GGTCTTGTTtGCCGcCGCATACTTtGCGTCgGCcGCcAACTGGGCTAAGGTaGTGCTGGTt
47	SA5	489 GGTCTTGTTcGCCGtCGCATACTTCGCGTCAGCGGCTAACTGGGCTAAGGTTGTGCTGGTC
49	SA7	489 GGTCTTGTTcGCCGCCGCATATTTCGCGTCAGCGGCTAACTGGGCTAAGGTTGTGCTGGTC
46	SA4	489 GGTCTTGTTtGCCGCCGCATATTTCGCGTCAGCGGCTAACTGGGCTAAGGTTaTaCTGGTC
50	SA13	489 GGTCTTGTTcGCCGCCGCATACTaCGCGTCGGCGGCTAACTGGGGcAAGGTTGTGCTGGTC
48	SA6	489 GGTCTTGTTcGCCCGtGCATACTtCGCGTCGGCGGCTAACTGGGctAAGGTTGTGCTGGTC
45-50	consensus	GGTCTTGTTcGCCGcCGCATACTtGCGTC - GCgGCTAACTGGGctAAGGTTgTgCTGGTc

<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	550 CTGTTcCTGTTTGCGGGGGTCGATGGC
47	SA5	550 CTGTTTCTGTTTGCGGGGGTCGATGGC
49	SA7	550 TTGTTTCTGTTTGCGGGGGTCGATGCC
46	SA4	550 TTGTTTCTGTTTGCGGGGGTCGATGCC
50	SA13	550 cTGTTTCTGTTTGCGGGGGTCGATGCC
48	SA6	550 tTGTTTCTGTTTGCGGGGGTcGATGCC
45-50	consensus	-TGTTtCTGTTTGCGGGGGTcGATGcC

FIGURE 1H

## SEQ ID NO: Genotype

30-33 (IV/2b)  
 34 (2c)  
 26-29 (III/2a)  
 35-39 (V/3a)  
 9-25 (II/1b)  
 1-8 (I/1a)  
 40 (4a)  
 42-43 (4c)  
 44 (4d)  
 41 (4b)  
 45-50 (5a)  
 51 (6a)

1-51 consensus

## SEQ ID NO: Genotype

30-33 (IV/2b)  
 34 (2c)  
 26-29 (III/2a)  
 35-39 (V/3a)  
 9-25 (II/1b)  
 1-8 (I/1a)  
 40 (4a)  
 42-43 (4c)  
 44 (4d)  
 41 (4b)  
 45-50 (5a)  
 51 (6a)

1-51 consensus

## SEQ ID NO: Genotype

30-33 (IV/2b)  
 34 (2c)  
 26-29 (III/2a)  
 35-39 (V/3a)  
 9-25 (II/1b)  
 1-8 (I/1a)  
 40 (4a)  
 42-43 (4c)  
 44 (4d)  
 41 (4b)  
 45-50 (5a)  
 51 (6a)

1-51 consensus

1 GTGGAAGTcAGgAACAtCAGTTctAGcTACTAcGCCACCAATGATTGCTCaAACaACAGCA  
 1 GTGGAGGTCAAGGACACCGGCGACTCCTACATGCCGACCAACGATTGCTCCAACCTCTAGTA  
 1 GcccAAGTGAagAACACCAgtacCaGcTAcATGGTGACcAACGACTGtTCcAAtGAcAGCA  
 1 cTAGAGTGGCGGAATaCGTctGGCCTCTAtgTCCTtACCAACGACTGtTCCAATAGCAGTA  
 1 tAtGAaGTGCgCAACGTgTCCGGGgtgTAccAtGTCACgAACGACTGcTCCAACtcaAGca  
 1 tACCAAGTgCGCAACTCcaCgGGgCTtTACCATGTcACCAATGAtTGCCCTAAcTCGAGtA  
 1 GAGCACTACCGGAATGCTTCGGGCATCTATCACATCACCATGATTGTCCGAATTCCAGTA  
 1 GTtAACTATCgCAATGCCTCGGGCGTCTATCACgTCACCAACGACTGCCCGAACTCGAGCA  
 1 TACAACtATCGCAACAGCTCGGGTGTCTACCATGTCACCAACGATTGCCCGAACTCGAGCA  
 1 GTGCACTACCGGAATGCTTCGGGCATCTATCATGTcACCAATGATTGCCcCAACTCtTCCA  
 1 GTtCCcTACCGaAAtGCCTCtGGGGTtTAtCATGTcACCAATGAtTGCCcCAACTCtTCCA  
 1 CTTACCTACGGCAACTCCAGTGGGCTATACCATCTCACAATGATTGCCcCAACTCCAGCA

A

TA

AC AA GA TG C AA

62 TCACCTGGCAaACTCACCaaACGCAgttCTCCACCTTCCCGGATGCGTCCCaTGTGAGAATGA  
 62 TCGTTTGGCAGCTTGAAGGAGCAGTGCTTCATACTCCTGGATGCGTCCCTTGTGAGCGTAC  
 62 TCACcTGGCAaACTccAgGCcCGGGTcCTCCACGTcCCCGGGTgTgTCCCGTGcGAGAAagt  
 62 TtGTGTATGAGGCCGATGACGTcATTCTGCACACACcTGGCTGTGTACCTTGTGTTCAGGA  
 62 TtGTGTatGAggCAgCgGACaTGATcaTGCAcACcCCcGGgTGcgtTgCCCTGcGTtCgGGA  
 62 TtGTGTACGAGgCgGCcGATgCAtcCTgCacaCtCCgGGgTGTGTcCCTTGCgTTCGcGA  
 62 TAGTCTATGAAGCTGACCATCACATCTACACTTGCCGGGTGCGTACCCTGTGTGATGAC  
 62 TAgtGTATGAGGCCGAACACCagATCtTACACCTCCCGGGTGTGCTTGTGTGATGAGGt  
 62 TAGTCTATGAAACCGATTACCACATCTTACACCTCCCGGGATGCGTTCCTTGCgTGAGGGa  
 62 TAGTGTACGAGACGGAGCACCACATCATGCACTTGCCAGGGTGTGTCCCTGTGTGCGGAC  
 62 TaGTcTAcGAGGCTGAtaaCCTGATctTgCAcGCACCTGGtTGCGTGCCcTGTGTcaggca  
 62 TCGTGCTGGAGGCGGATGCTATGATCTTGcATTGCGCTGGATGCTTGCCTTGTGTGAGGGT

T

A

T T CA

CC GG TG T CC TG G

123 cAATGGCACCCcTGCgCTGCTGGATACAAGTgACACCTAATGTGGCTGTGAAACACCGcGGC  
 123 CGCCAACGTCTCTCGATGTTGGGTGCCGGTTGCCcCAATCTCGCCATAAGTCAACCTGGC  
 123 gGGAAAtaCaTcTcGgTGCTGGATACCGGTctCaCCAAAcGTgGCcGTGCaGCaGCCcGGC  
 123 CGGcAATACATCcAcGTGCTGGACCCcAgTGACaCCTACaGTGGCAGTCAGGTAcGTcCGGA  
 123 gaacAActcCTCccgcTGcTGGGTaGCGCTcaCtCCcACgCTcGCgGCcAGGAAcgcAgC  
 123 GGgTaaCgcctCGAggTGTGGGTGgCGgTGaCCCCCACgGTgGCCACcAGGGAcGGCAaA  
 123 TGGGAACACATCGCGTGTGCTGGACGCCGTGACGCCTACAGTGGCTGTGCGCACACCCGGGC  
 123 tGGGAAtCAGTCACGCTGCTGGGTGGCCCTTACTCCCACCGTGGCGGtGtCTTATATCGGT  
 123 AGGGAACAAGTCTACATGCTGGGTGTCTCTACCCCCACCGTGGCTGCGCAACATCTGAAT  
 123 GGAGAATACTTCTCGCTGCTGGGTGCCCTTGACCCCCACTGTGGCCGCGCCCTATCCCAAC  
 123 agaTAATGTcAGTAggTGCTGGGTcCAaATCACCCCCACatTgTCAGCCCCGAaccTCGGA  
 123 CGATGATCGGTCCACCTGTTGGCATGCTGTGACCCCCACCGTGGCCATACCAATGCTTCC

TG TGG

T C CC A T C

FIGURE 1H

SEQ ID NO:	Genotype	
30-33	(IV/2b)	184 GCaCTcACTCacAACCTGCGAaCaCATgTcGacaTGATcGTAATGGCAGCTACGGTCTGCT
34	(2c)	184 GCTCTCACTAAGGGCCCTGCGAGCACACATCGATATCATCGTGATGTCTGCTACGGTCTGTT
26-29	(III/2a)	184 GCcCTcACGCAGGGCTTGGCGACgCACATcGACATGGTtGTGATGTCCGCCACGCTCTGCT
35-39	(V/3a)	184 GCAACCACCGCtTCGATACGCAGTCATGTGGACCTatTaGTGGGCGCGGCCACgaTGTGCT
9-25	(II/1b)	184 gTCcCcActAcGaCaATACGACgcCAcGTcGAtTTGCTCGTTGGGGCGGCTgctTTCTGcT
1-8	(I/1a)	184 CTCCCCgCAaCGCAGCTtCGACGTcACATCGAtCTGCTtGTcGGgAGcGCCACCCTCTGcT
40	(4a)	184 GCTCCGCTTGAGTCGTTCCGGCGACATGTGGACTTAATGGTAGGGCGCGCCACTTTGTGTT
42-43	(4c)	184 GCTCCGCTTGAGTCCTTTGAGACGTACGTGGATCTGATGGTGGGCGGCCACTCTCTGCT
44	(4d)	184 GCTCCGCTTGAGTCCTTTGAGACGTACGTGGATCTGATGGTGGGCGGCCACTCTCTGCT
41	(4b)	184 GCACCGTTAGAGTCCATGCGCAGGCATGTAGACCTGATGGTGGGTGCGGCTACTATGTGTT
45-50	(5a)	184 GCGGTCACGGCTCCTCTTCGGAGGGcCGTTGAcTAcTaGCGGGaGGgGCTGcCCTcTGCT
51	(6a)	184 ACGCCCCGAACGGGATTCCGCAGGCATGTGGATCTTCTTGCGGGCGCCGAGTGGTTTGCT
1-51	consensus	T G T GA T G GC T TG T
SEQ ID NO:	Genotype	
30-33	(IV/2b)	245 CGGCCTTGATGTGGGaGACgTgTGCGGGGGCCGTGATGATcGtGTCGCAGGCTtTCATAaT
34	(2c)	245 CTGCCCTTTATGTGGGGGACGTGTGTGGCGCGCTGATGCTGGCCGCTCAGGTCGTCTGCT
26-29	(III/2a)	245 CcGCTcTtTACGTGGGGGAaccTCTGCGGcGGGgTgATGCTCGCaGCcCaGATGTTcATgt
35-39	(V/3a)	245 CTGCGCTCTAcGTGGGtGATaTGTGTGGGGCCGTCTTtCTcGTGGGACAAGCCTTCACGTT
9-25	(II/1b)	245 CCGctATGTAcGTGGGgGATcTcTGCGGaTcTGTtTCCTcGTcTcCAGcTGTTCACctT
1-8	(I/1a)	245 CGGCCCTCTAcGTGGGGGACTGTGCGGGTCTGTCTTtCTtGTcGtCaACTGTTcACctT
40	(4a)	245 CTGCCCTCTATGTTGGGGACCTCTGCGAGGTGCTTCTGATGGGGCAGATGATCACTTT
42-43	(4c)	245 CtGCCCTCTACgTTGGaGATcTGTGCGGTGGtGcATTCTTGGTTGGcCAGATGTTcTCcTT
44	(4d)	245 CCGCCCTCTACATCGGAGACGTGTGTGGGGGTGTGTTCTTGGTGGTCAACTGTTcACCTT
41	(4b)	245 CCGCCTTCTACATTGGAGATCTGTGTGGAGGCGTCTTCTAGTGGGGCAGCTGTTTCGACTT
45-50	(5a)	245 CCGCgCTATACGTCCGGgGACGcGTGCGGGGcAgTGTtTtTGGTAGGcCaATGTTcAcCTA
51	(6a)	245 CATCCCTGTACATCGGGGACCTGTGTGGCTCTCTTTTTGGCGGGACAACCTATTACCTT
1-51	consensus	C T TA T GG GA TG GG T T CA T
SEQ ID NO:	Genotype	
30-33	(IV/2b)	306 ATCGCCaGAACgCCACaACTTtACCCaAGAGTGCAACTGTTCCATCTACCAAGGTCatATC
34	(2c)	306 GTCGCCACAACACCATAACGTTTGTCCAGGAATGCAACTGTTCCATATACCCGGGCGCATT
26-29	(III/2a)	306 CTCGCCGCaACacCACTgGTTTGTGCaAGaTGCAATTGCTCcAtcTACCctGGtACCATC
35-39	(V/3a)	306 CAGACCTcGTTCGCCATCAAAcGTTCAGACCTGTAACTGCTCGCTGTACCCAGGCCAtcTT
9-25	(II/1b)	306 cTCgCCTcGcCggcAtgaGACagtaCAGgAcTGcAAcTGcTcaTCTATCCcGGcCacgTa
1-8	(I/1a)	306 cTCTCCAGgCgCCaCTGGACaACGCaAGaCTGcAAcTGTtTcTATcTCCcGGCCaTaTa
40	(4a)	306 TCGGCCCGCTCGCCACTGGACCACGCAGGAGTGCAATTGTTCCATCTACACTGGCCATATC
42-43	(4c)	306 CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCTATCTAcGCaGGGCataTc
44	(4d)	306 CCAACCTCGCCGCCACTGGACCACCCAGGATTGCAACTGCTCCATCTATCCTGGTCACGTC
41	(4b)	306 CCGACCGCGCCGGCACTGGACCACCCAGGATTGCAACTGCTCCATCTATCCTGGTCACGTC
45-50	(5a)	306 TAGgCCTCGCCaGCaTactacgGTgCAGGACTGCAAcTGTtTcATTtACAGtGGCCatATC
51	(6a)	306 TCAGCCCCCGCGTCATTGGACTGTGCAAGACTGCAACTGCTCCATCTATACAGGCCACGTC
1-51	consensus	CC C CA TG AA TG TC T TA GG T
SEQ ID NO:	Genotype	
30-33	(IV/2b)	367 ACCGGCCACCGCATGGCaTGGGACATGATGCTaAACTGGTCACCAACTCTtACCATGATCC
34	(2c)	367 ACGGGACACCGCATGGCTTGGGATATGATGATGAACCTGGTCGCCCCACTACCACCATGCTCC
26-29	(III/2a)	367 ActGGaCACCGTATGGCATGGGaCATGATGATGAACCTGGTCGCCCCACgGCACcaTGATCc
35-39	(V/3a)	367 TCAGGACATCGaATGGCTTGGGATATGATGATGAATTGGTCCCCCGCtGTGGGTATGGTGG
9-25	(II/1b)	367 tCAGGTcAcCGcATGGCtTGGGAtATGATGATGAACCTGGTCaCCTACAgCaGCcTaGTgg
1-8	(I/1a)	367 ACGGGtCaCCGcATGGCaTGGGATATGATGATGAACCTGGTCCCCtACGaCgGCcTGGTAg
40	(4a)	367 ACCGGCCACAGGATGGCTGGGACATGATGATGAACCTGGAGCCCTACCACCCTCTGCTCC
42-43	(4c)	367 ACgGGCCACAGgATGGCATGGGACATGATGATGAACCTGGAGTCCcACAACCACcTGTcTc
44	(4d)	367 ACAGGACACAGAATGGCTTGGGACATGATGATGAACCTGGAGCCCTACCAGCGCGCTGATTA
41	(4b)	367 TCGGGCCACAGGATGGCTTGGGACATGATGATGAATTGGAGCCCCACTGCGACGCTGGTCC
45-50	(5a)	367 ACcGGCCACCGgATGGCaTGGGACATGATGATGAATTGGTCACCTaCgACaGcTTGgTGA
51	(6a)	367 ACCGGCCACAGGATGGCTTGGGACATGATGATGAACCTGGTCACCCACAACCCTCTGGTCC
1-51	consensus	C GG CA G ATGGC TGGGA ATGATG T AA TGG CC C T T

FIGURE 1H

SEO ID NO:    Genotype

30-33    (IV/2b)  
       34    (2c)  
 26-29    (III/2a)  
 35-39    (V/3a)  
       9-25    (II/1b)  
       1-8    (I/1a)  
       40    (4a)  
 42-43    (4c)  
       44    (4d)  
       41    (4b)  
 45-50    (5a)  
       51    (6a)

1-51    consensus

428 TcGCCTAtGcCGcTcGTGTtCCTGAgCTAGtCCTtgAaGTtGTCTTCGGcGGcCATTGGGG  
 428 TGGCGTACTTGGTGCGCATCCCGGAAGTCATCTTGGATATTGTTACAGGAGGTCAATTGGGG  
 428 TGGCGTACGcGATGCGCGTTCCTCGAGGTCACTaTAGACATCaTtaGCGGgGCTCACTGGGG  
 428 TgGCGCACgTcCTGCGtTGCCCCAGACcTGTTcGACATAaTaGcCGGGGCCCACTGGGG  
 428 TaTCGCAgtTaCTCCGgaTCCCaCAAGCTgTCgTGGAcATGGTggCgGGgGCCCACTGGGG  
 428 TaGCTcAGCTGCTCcGGaTCCCGCAaGCCaTCTTGGAcATGATCGCTGGtGCcCACTGGGG  
 428 TCGCCcAGATCATGAGGGTCCCCACAGCCTTTCTCGACATGGTTGCCGAGGCCACTGGGG  
 428 TCGCCcAGGTcATGAGGATCCCTAGCACTCTGGTAgAtCTACTCgCTGGAGGGCACTGGGG  
 428 TCGCCcAACTTATGAGGATCCcAGGCGCCATGGTCGACCTGCTTGCAGGCGGCCACTGGGG  
 428 TGGCTCAGATCTTACGGATCCCTCTATCTAGGTGACTTGCTCACCGGGGGTCACTGGGG  
 428 TGGCCcAgTgTcTACGGATtCCCCAgGTGGTCATtGACATCATtGCCGGGGgCCACTGGGG  
 428 TATCTAGCATCTTGAGGGTACCTGAGATTTGTGCGAGTGTGATATTTGGTGGCCATTGGGG

T   C                    G   T   CC                    T   T                    GG   G   CA   TGGG

SEO ID NO:    Genotype

30-33    (IV/2b)  
       34    (2c)  
 26-29    (III/2a)  
 35-39    (V/3a)  
       9-25    (II/1b)  
       1-8    (I/1a)  
       40    (4a)  
 42-43    (4c)  
       44    (4d)  
       41    (4b)  
 45-50    (5a)  
       51    (6a)

1-51    consensus

489 cGTGGTGTtTGGCTTGGCCTATTTCTCCATGCAgGGAGCGTGGGCCAAaGTCATtGCCATC  
 489 TGTAATGTtTGGCCTCGCTTACTTCTCCATGCAAGGATCGTGGGCGAAGGTCACTCGTTATC  
 489 CGTCaTGTTcGGCtTaGCCTACTTCTCTATGCAAGGAGCGTGGGCGAAaGTCgTTGTATC  
 489 CATctTGGCgGGCCTAGCCTATTaTcCaATGCAgGGCAACTGGGCCAAGGTGCTATcaTC  
 489 agTCCTgCGGGCCTtGCcTACTAtTCCATGGtggGgAACTGGGCTaAGGTtTgATTGTg  
 489 AGTCCTaCGGGCATAGCGTATTtTCCATGGtGGGgAACTGGGCGAAGGTCCtTgTAgTg  
 489 CGTCCTCGCGGGCTTGGCGTACTTcAGCATGCAAGGCAATTGGGCCAAGGTAGTCCTGGTC  
 489 cgTCCTTgTtGGGtTGGCgTACTTcAgAtATGCAAGCTAATTGGGCCAAaGTCATcCTGGTC  
 489 CATTCTGGTTGGCATAGCGTACTTcAGCATGCAAGCTAATTGGGCCAAGGTATCCTGGTC  
 489 AGTTCTTGCTGGTCTAGCTTTCTTcAGCATGCAAGGTAAGTGGGCGAAGGTATCCTGGTC  
 489 GGTCTTGTtTcGCCGcCGCATAcTtCGGCTCgGCgGCTaACTGGGCTaAGGTtTgTgCTGGTc  
 489 GATACTACTAGCCGTTGCCTACTTTGGCATGGCTGGCAACTGGCTAAAAGTTCTGGCTGTT

T   T                    G                    GC   T   T                    TGG   AA   GT                    T

SEO ID NO:    Genotype

30-33    (IV/2b)  
       34    (2c)  
 26-29    (III/2a)  
 35-39    (V/3a)  
       9-25    (II/1b)  
       1-8    (I/1a)  
       40    (4a)  
 42-43    (4c)  
       44    (4d)  
       41    (4b)  
 45-50    (5a)  
       51    (6a)

1-51    consensus

550 CTCCTtCTTGTcGCAGGAGTGGAtGCA  
 550 CTCCTGCTGACTGCTGGGGTGGAGGCG  
 550 CTtTGCTggCcGCTGGgGTGGACGCG  
 550 ATGgTTATGTTTTcAGGgGTcGAtGCC  
 550 aTGCTACTcTTTGCcGGcGtTGAcGGg  
 550 CTGtTGCTgTtTgCCGGCGTcGAtGCG  
 550 CTTTTCTCTTTGCTGGGGTAGACGCC  
 550 CTTTTCTCTcCGCTGGAGTTGATGCC  
 550 CTGTTTCTCTTTGCTGGAGTCGACGCT  
 550 CTATTCCTCTTTGCCGGGGTCGAGGGA  
 550 tTGTTtCTGTTTGCGGGGTcGATGcC  
 550 CTGTTCTATTtGCAGGGGTTGAAGCA

T   T   T                    C   GG   GT   GA   G

FIGURE 2A

<u>SEQ ID NO:</u>	<u>Isolate</u>	
56	S14	1 YQVRNSTGLYHVTNDCPNSSIVYEtADAILHaPGCVPCVREGNtSRCWVAMTPTVATRDGK
52	DK7	1 YQVRNSTGLYHVTNDCPNSSIVYEADAILHTPGCVPCVREGNvSRCWVAMTPTVATRDGK
59	US11	1 YQVRNSTGLYHVTNDCPNSSIVYEADAILHTPGCVPCVREGNaSRCWVAMTPTVATRDGK
55	DR4	1 HQVRNSTGLYHVTNDCPNSSIVYEADAILHTPGCVPCVREGNtSRCWVAVTPTVATRDGK
54	DR1	1 HQVRNSTGLYHVTNDCPNSSIVYEADAILHaPGCVPCVREGNASRCWVAVTPTVATRDGK
53	DK9	1 YQVRNSSGLYHVTNDCPNSSIVYEADAILHSPGCVPCVREGNASKCWVAVAPTPTVATRDGK
58	SW1	1 YQVRNSSGLYHVTNDCPNSSIVYETADAILHSPGCVPCVREdGApKCWVAVAPTPTVATRDGK
57	S18	1 YQVRNSTGLYHVTNDCPNSSIVYETADtILHSPGCVPCVREGnAsrCWVpVAPTPTVATRDGK
52-59	consensus	yQVRNSTGLYHVTNDCPNSSIVYEaADaILH - PGCVP CVREgnaSrCWVavtPTVATRDGK

<u>SEQ ID NO:</u>	<u>Isolate</u>	
56	S14	62 LPatQLRRyIDLLVGSATLCSALYVGDLGGSVFLVGQLFTFSPrRlWTTQdCNCsIYPGHI
52	DK7	62 LPTaQLRRHIDLLVGSATLCSALYVGDLGGSVFLVGQLFTFSPrRHWTtQGCNCsIYPGHI
59	US11	62 LPTTQLRRHIDLLVGSATLCSALYVGDLGGSVFLVGQLFTFSPrRHWTtQGCNCsIYPGHI
55	DR4	62 LPTTQLRRHIDLLVGSATLCSALYVGDLGGSVFLVGQLFTFSPrRhWTTQdCNCsIYPGHI
54	DR1	62 LPTTQLRRHIDLLVGSATLCSALYVGDLGGSVFLVGQLFTFSPrRHWTtQdCNCsIYPGHI
53	DK9	62 LPATQLRRHIDLLVGSATLCSALYVGDLGGSVFLVGQLFTFSPrRHWTtQdCNCsIYPGHI
58	SW1	62 LPATQLRRHIDLLVGSATLCSALYVGDLGGSVFLVSQLFTFSPrRHWTtQdCNCsIYPGHI
57	S18	62 LPATQLRRHIDLLVGSATLCSALYVGDLGGSVFLVSQLFTiSPRRHWTtQdCNCsIYPGHI
52-59	consensus	LP - tQLRRHIDLLVGSATLCSALYVGDLGGSVFLvgQLFTfSPRRhWTTQdCNCsIYPGHI

<u>SEQ ID NO:</u>	<u>Isolate</u>	
56	S14	123 TGHrMAWdMMNWSPTTALVVAQLLRiPQaiLDmiAGAHGVLAGIAYFSMvGNWAKVLvV
52	DK7	123 TGHrMAWdMMNWSPTTALVVAQLLRiPQaiLDmiAGAHGVLAGIAYFSMvGNWAKVLvV
59	US11	123 TGHrMAWdMMNWSPTaALVVAQLLRiPQaiLDmiAGAHGVLAGIAYFSMvGNWAKVLvV
55	DR4	123 TGHrMAWdMMNWSPTTALVVAQLLRiPQaiLDmiAGAHGVLAGIAYFSMvGNWAKVLvV
54	DR1	123 TGHrMAWdMMNWSPTTALVMAQLLRiPQaiLDmiAGAHGVLAGIAYFSMvGNWAKVvVv
53	DK9	123 TGHrMAWdMMNWSPTaALVMAQLLRiPQaiLDmiAGAHGVLAGIAYFSMvGNWAKVvVv
58	SW1	123 TGHrMAWdMMNWSPTTALVvAQLLRiPQAVLDmiAGAHGVLAGIAYFSMvGNWAKVLiV
57	S18	123 TGHrMAWdMMNWSPTTALViAQLLRvPQAVLDmiAGAHGVLAGIAYFSMaGNWAKVLiV
52-59	consensus	TGHrMAWdMMNWSPTtALVvAQLLRiPQaiLDmiAGAHGVLAGIAYFSMvGNWAKVLvV

FIGURE 2A

<u>SEQ ID NO:</u>	<u>Isolate</u>		
56	S14	184	LLLFAGVDA 
52	DK7	184	LLLFAGVDA 
59	US11	184	LLLFAGVDA 
55	DR4	184	LLLFAGVDA 
54	DR1	184	LLLFAGVDA 
53	DK9	184	LLLFtGVDA 
58	SW1	184	LLLFsGVDA 
57	S18	184	LLLFaGVDA 
52-59	consensus		LLLFaGVDA

0004591-052590

FIGURE 2B

SEQ ID NO:	Isolate	
75	T10	1 YEVRNVSGmYHVTNDCSNSSIVFEAdlIMHTPGCVPCVREgNsSRCWVALTPTLAARNtS
62	DK1	1 YEVRNVSGvYHVTNDCSNSSIVYEAAdvIMHTPGCVPCVRENNhSRCWVALTPTLAARNAS
64	HK4	1 hEVhNVSGiYHVTNDCSNSSIVYEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNAS
76	US6	1 YEVRNVSGmYHVTNDCSNSSIVYEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNAS
68	IND8	1 YEVRNVSGVYHVTNDCSNSSIVYEAADMIMHTPGCVPCVREgNfSsCWVALTPTLAARNAS
67	IND5	1 YEVRNVSGVYHVTNDCSNSSIVYEAADMIMHTPGCVPCVREgNSSRCWVALTPTLAARNAS
73	SW2	1 YEVRNVSGVYHVTNDCSNSSIVYETADMIMHTPGCVPCVREaNSSRCWVALTPTLAARNtS
63	HK3	1 YEVRNVSGiYHVTNDCSNSSvVYETADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNVS
66	HK8	1 YEVRNVSGiYHVTNDCSNSSIVYETADMIMHTPGcmPCVRENNSSRCWVALTPTLAARNVS
61	D3	1 YEVRNVSGVYqVTNDCSNSSIVYETADMIMHTPGCVPCVREdNSSRCWVALTPTLAARNsS
74	T3	1 YEVRNVSGVYyVTNDCSNSSIVYETADMIMHTPGCVPCVREsNSSRCWVALTPTLAARNAS
65	HK5	1 YEVRNVSGVYHVTNDCSNlSIVYETtDMIMHTPGCVPCVRENNSSRCWVALaPTLAARNAS
71	S45	1 YEVRNVSGaYHVTNDCSNSSIVYEAAdvIlHTPGCVPCVRENNSSRCWVALTPTLAARNSS
72	SA10	1 YEVRNVSGmYHVTNDCSNSSIVYEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNSS
69	P10	1 YEVRNVSGVYHVTNDCSNSSIVYEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNSS
60	D1	1 YEVRNVSGVYHVTNDCSNSSIVYEtADMIMHTPGCVPCVREdNSSRCWVALTPTLAARNgn
70	S9	1 YEVRNVSGaYHVTNDCSNSSIVYEAAdvIMHTPGCVPCVqEgNSSqCWVALTPTLAARNat
60-76	consensus	yEVrNVSGvYhVTNDCSNsSiVyEaaDmImHTPGCVPCVrEnNsSrCWVALtPTLAARNas



FIGURE 2B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
75	T10	62 vPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRRHETlQDCNCsIYPGHl
62	DK1	62 IPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRRHETaQDCNCsIYPGHV
64	HK4	62 IPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRRHETVQDCNCsIYPGHV
76	US6	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLiSQLFTFSPPRqHETVQDCNCsIYPGHV
68	IND8	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRRHETVQDCNCsIYPGHV
67	IND5	62 VsTTTIRrhVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRRHETVQDCNCsIYPGHV
73	SW2	62 VPTTTIRRHVDLLVGAAAFCSvMYVGDL CGSVFLVSQLFTFSPPRRHETVQDCNCsIYPGHV
63	HK3	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRRHETVQDCNCsIYPGHV
66	HK8	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRRHETVQDCNCsIYPGHV
61	D3	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRRHETVQeCNCsIYPGHV
74	T3	62 VPTkTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRRHETVQDCNCsIYPGHV
65	HK5	62 VPTTaIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRRHETVQDCNCsIYPGHV
71	S45	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRRHETVQDCNCsIYPGHV
72	SA10	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRRyETVQDCNCsIYPGrV
69	P10	62 VPTTAIRRHVDLLVGAAAFCSAMYVGDL CGSVlLVSQLFTFSPPRRhwTVQDCNCsIYPGHV
60	D1	62 VPTTAIRRHVDLLVGAAAFCSAMYVGDL CGSVFLiSQLFTlSPRRHETVQeCNCsIYPGHV
70	S9	62 VPTTtIRRHVDLLVGAAvFCSAMYVGDL CGSVFLiSQLFTiSPRRHETVQnCNCsIYPGHV
60-76	consensus	vpTtTIRrHVDLLVGAAaFCSaMYVGDL CGSVfLVSQLFTfSPRRheTVQdCNCsIYPGHv

FIGURE 2B

SEQ ID NO:	Isolate	
75	T10	123 SGHRMAWDMMMNWSPTTALVvSQLLRIPQAVmDMVtGAHWGVLAGLAYYSMAGNWAKVLI
62	DK1	123 SGHRMAWDMMMNWSPTTALVLSQLLRIPQAVvDMVAGAHWGVLAGLAYYSMAGNWAKVLI
64	HK4	123 SGHRMAWDMMMNWSPTAALVVSQLLRlPQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLI
76	US6	123 SGHRMAWDMMMNWSPTAALVVSQLLRIPQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLI
68	IND8	123 SGHRMAWDMMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGILAGLAYYSMVGNWAKVLI
67	IND5	123 SGHRMAWDMMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGILAGLAYYSMVGNWAKVLI
73	SW2	123 SGHRMAWDMMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
63	HK3	123 SGHRMAWDMMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
66	HK8	123 SGHRMAWDMMMNWSPTtALVVSQLLRIPQAIvDMVAGAHWGVLAGLAYYSMVGNWAKVLI
61	D3	123 TGHRMAWDMMMNWSPTaALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
74	T3	123 TGHRMAWDMMMNWSPTTALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
65	HK5	123 TGHRMAWDMMMNWSPTTALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
71	S45	123 TGHRMAWDMMMNWSPTaALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
72	SA10	123 TGHRMAWDMMMNWSPTtALVVSQLLRIPQAIvDMVAGAHWGVLAGLAYYSMVGNWAKVLI
69	P10	123 sGHRMAWDMMMNWSPTaALVVSQLLRIPQAIldvVAGAHWGVLAGLAYYSMVGNWAKVLI
60	D1	123 TGHRMAWDMMMNWSPTTALVVSQLLRIPQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLI
70	S9	123 TGHRMAWDMMMNWSPTTALVVSQLLRIPQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLI
60-76	consensus	sGHRMAWDMMMNWSPTaALVvSQLLRiPQAVvDmVaGAHWGvLAGLAYYSMvGNWAKVLI

FIGURE 2B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
75	T10	184 mLLFAGVDG 
62	DK1	184 lLLFAGVDG 
64	HK4	184 mLLFAGVDG 
76	US6	184 lLLFAGVDG 
68	IND8	184 MLLFAGVDG 
67	IND5	184 MLLFAGVDG 
73	SW2	184 MLLFAGVDG 
63	HK3	184 MLLFAGVDG 
66	HK8	184 MLLFAGVDG 
61	D3	184 MLLFAGVDG 
74	T3	184 lLLFAGVDG 
65	HK5	184 MLLFAGVDG 
71	S45	184 MLLFAGVDG 
72	SA10	184 MLLFAGVDG 
69	P10	184 MLLFAGVDG 
60	D1	184 MLLFAGVDG 
70	S9	184 MLLFAGVDG 
60-76	consensus	mLLFAGVDG

FIGURE 2C

<u>SEQ ID NO:</u>	<u>Isolate</u>	
77	T2	1 AQVrNTsrgYMTNDCSNeSITWQLQAAVLHVPGCiPCErlGNTSRCWIPVtPNVAVRQPG
78	T4	1 AQVKNTtnSYMTNDCSNDsITWQLQAAVLHVPGCVPCEktGNTSRCWIPVSPNVAVRQPG
79	T9	1 AeVKNTSTSYMTNDCSNDsITWQLQAAVLHVPGCVPCErVGNaSRCWIPVSPNVAVRQPG
80	US10	1 vqVKNTSTSYMTNDCSNDsITWQLLeAAVLHVPGCVPCEkVGntSRCWIPVSPNVAVRQPG
77-80	consensus	aqVKNtstsYMTNDCSNDsITWQLqAAVLHVPGCvPCE-vGntSRCWIPVsPNVAV--PG
<u>SEQ ID NO:</u>	<u>Isolate</u>	
77	T2	62 ALTQGLRTHIDMVMSATLCSALYVGDLCCGVMLAAQMFIvSPrrHWFVQeCNCSIYPGTI
78	T4	62 ALTQGLRTHIDMVMSATLCSALYVGDLCCGVMLAAQMFIvSPQHHWFVQdCNCSIYPGTI
79	T9	62 ALTQGLRTHIDMVMSATLCSALYVGDLCCGVMLAAQMFIiSPQHHWFVQECNCSIYPGTI
80	US10	62 ALTQGLRTHIDMVMSATLCSALYVGDLCCGVMLAAQMFIvSPrHhSFVQECNCSIYPGTI
77-80	consensus	ALTQGLRTHIDMVMSATLCSALYVGDLCCGVMLAAQMFIvSP-hHwFVQeCNCSIYPGTI
<u>SEQ ID NO:</u>	<u>Isolate</u>	
77	T2	123 TGHrMAWDMMNWSPTATMILAYAMRVPEVIiDiigGAHWGVmFGLAYFSMQAWAKViVi
78	T4	123 TGHrMAWDMMNWSPTATMILAYAMRVPEVIIdIvSGAHWGVmFGLAYFSMQAWAKVVVI
79	T9	123 TGHrMAWDMMNWSPTtTMILAYAMRVPEVIIDIISGAHWGVmFGLAYFSMQAWAKVVVI
80	US10	123 TGHrMAWDMMNWSPTaTlILAYvMRVPEVIIDIISGAHWGVlFGLAYFSMQAWAKVVVI
77-80	consensus	TGHrMAWDMMNWSPTaTmILAYaMRVPEVIiDiisGAHWGVmFGLAYFSMQAWAKVvVI
<u>SEQ ID NO:</u>	<u>Isolate</u>	
77	T2	184 LLLAAGVDA
78	T4	184 LLLAAGVDA
79	T9	184 LLLtAGVDA
80	US10	184 LLLaAGVDA
77-80	consensus	LLLaAGVDA

FIGURE 2D

SEQ ID NO:    Isolate

82                    DK11

83                    SW3

84                    T8

81                    DK8

81-84                consensus

1 VEVNRtSSSYATNDCSNnSITWQLTNAVHLPGCVPCENDNGTLHCWIQVTPNVAVKHrg  
 |||||  
 1 VEVRNiSSSYATNDCSNnSITWQLTNAVHLPGCVPCENDNGTLHCWIQVTPNVAVKHrg  
 |||||  
 1 VEVNRtSfSYATNDCSNnSITWQLTNAVHLPGCVPCENDNGTLRCWIQVTPNVAVKHrg  
 |||||  
 1 VEVRNiSsSYATNDCSNnSITWQLTNAVHLPGCVPCENDNGTLRCWIQVTPNVAVKHrg  
 |||||  
 VEVRN-SsSYATNDCSNnSITWQLTNAVHLPGCVPCENDNGTL-CWIQVTPNVAVKHrg

SEQ ID NO:    Isolate

82                    DK11

83                    SW3

84                    T8

81                    DK8

81-84                consensus

62 ALTHNLRahIdMIVMAATVCSALYVGdVCGAVMIVSQAFIvSPEhHhFTQECNCsIYQGHrI  
 |||||  
 62 ALTHNLRahVdMIVMAATVCSALYVGdMCGAVMIVSQAFIISPERHNFTQECNCsIYQGrI  
 |||||  
 62 ALTHNLRTHVDVIVMAATVCSALYVGdVCGAVMIaSQAFIISPERHNFTQECNCsIYQGHrI  
 |||||  
 62 ALTHNLRTHVDVIVMAATVCSALYVGdVCGAVMIvSQALIISPERHNFTQECNCsIYQGHrI  
 |||||  
 ALTHNLR-HvD-IVMAATVCSALYVGdVCGAVMIvSQAFIISPERHhFTQECNCsIYQGHrI

SEQ ID NO:    Isolate

82                    DK11

83                    SW3

84                    T8

81                    DK8

81-84                consensus

123 TGHRMAWDMMLNWSPTLTMI LAYAArVPELVLEVVFgGHwGVVfGLAYfSMQgAWAKVIAI  
 |||||  
 123 TGHRMAWDMMLNWSPTLTMI LAYAArVPELVLEVVFgGHwGVVfGLAYfSMQgAWAKVIAI  
 |||||  
 123 TGHRMAWDMMLNWSPTLTMI LAYAArVPELVLEVVFgGHwGVVfGLAYfSMQgAWAKVIAI  
 |||||  
 123 TGHRMAWDMMLNWSPTLTMI LAYAArVPELaLqVVfGHwGVVfGLAYfSMQgAWAKVIAI  
 |||||  
 TGHRMAWDMMLNWSPTLTMI LAYAArVPELVLeVVfGHwGVVfGLAYfSMQgAWAKVIAI

SEQ ID NO:    Isolate

82                    DK11

83                    SW3

84                    T8

81                    DK8

81-84                consensus

184 LLLVAGVDA  
 |||||  
 184 LLLVAGVDA  
 |||||  
 184 LLLVAGVDA  
 |||||  
 184 LLLVAGVDA  
 |||||  
 LLLVAGVDA

09084691.052698

FIGURE 2E

SEQ ID NO:   Isolate

86                      DK12

87                      HK10

88                      S2

90                      S54

89                      S52

86-90                  consensus

1 LEWRNVSGLYVLTNDCCNSSIVYEADDVILHTPGCVPCVQDGNTSTCWTSPVTPTVAVRYVG  
 |||||  
 1 LEWRNVSGLYVLTNDCCNSSIVYEADDVILHTPGCVPCVQDGNTSTCWTSPVTPTVAVRYVG  
 |||||  
 1 LEWRNTSGLYVLTNDCCNSSIVYEADDVILHTPGCVPCVQDGNTSTCWTSPVTPTVAVRYVG  
 |||||  
 1 LEWRNTSGLYiLTNDCCNSSIVYEADDVILHTPGCVPCVQDGNTSTCWTSPVTPTVAVRYVG  
 |||||  
 1 LEWRNTSGLYvLTNDCCNSSIVYEADDVILHTPGCVPCVQDGNTSmCWTSPVTPTVAVRYVG  
 |||||  
 LEWRNtSGLYvLTNDCCNSSIVYEADDVILHTPGCVPCVQDGNTStCWTpVTPTVAVRYVG

SEQ ID NO:   Isolate

86                      DK12

87                      HK10

88                      S2

90                      S54

89                      S52

86-90                  consensus

62 ATTASIRSHVDLLVGAATMCSALYVGDvCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL  
 |||||  
 62 ATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL  
 |||||  
 62 ATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL  
 |||||  
 62 ATTASIRSHVDLLVGAATLCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL  
 |||||  
 62 ATTASIRSHVDLLVGAATLCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHv  
 |||||  
 ATTASIRSHVDLLVGAATmCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL

SEQ ID NO:   Isolate

86                      DK12

87                      HK10

88                      S2

90                      S54

89                      S52

86-90                  consensus

123 SGHRMAWDMMNWSPAVGMVVAHVLRPLPQTLFDIIAGAHWGImAGLAYYSMQGNWAKVAII  
 |||||  
 123 SGHRMAWDMMNWSPAVGMVVAHVLRPLPQTLFDIIAGAHWGILAGLAYYSMQGNWAKVAII  
 |||||  
 123 SGHRMAWDMMNWSPAVGMVVAHVLRPLPQTVFDIIAGAHWGILAGLAYYSMQGNWAKVAII  
 |||||  
 123 SGHRMAWDMMNWSPAVGMVVAHILRPLPQTLFDILAGAHWGILAGLAYYSMQGNWAKVAII  
 |||||  
 123 SGHRMAWDMMNWSPAVGMVVAHILRPLPQTLFDILAGAHWGILAGLAYYSMQGNWAKVAIv  
 |||||  
 SGHRMAWDMMNWSPAVGMVVAHVLRPLPQTLFDIIAGAHWGILAGLAYYSMQGNWAKVAii

SEQ ID NO:   Isolate

86                      DK12

87                      HK10

88                      S2

90                      S54

89                      S52

86-90                  consensus

184 MVMFSGVDA  
 |||||  
 184 MVMFSGVDA  
 |||||  
 184 MVMFSGVDA  
 |||||  
 184 MIMFSGVDA  
 |||||  
 184 MIMFSGVDA  
 |||||  
 MvMFSGVDA

**FIGURE 2F**

SEQ ID NO: Isolate  
94 27

94 27

93 26

93-94 consensus (26)

1 VNYhNASGVYHtTNDCPNSSImYEAEHhILHLP GCVP CVReGNQSRCWVALTPTVAAPYIG  
|||  
1 VNYrNASGVYHvTNDCPNSSIVYEAEHqILHLP GC l PCVRvGNQSRCWVALTPTVA v sYIG  
  
VNYrNASGVYHvTNDCPNSSIvYEAEHqILHLP GC l PCVRvGNQSRCWVALTPTVA v sYIG

SEQ ID NO: Isolate

94 27

93 26

93-94 consensus (Z6)

62 APLESiRRHVDLMVGAATVCSALYIGDLCGGVFLVGQMFsfQPRRHWTtQDCNCSIYAGHV  
|||  
62 APLdSLRRHVDLMVGAATVCSALYvGDLCGGaFLVGQMFsfQPRRHWTtQDCNCSIYAGHI  
  
APLdSlRRHVDLMVGAATVCSALYvGDLCGGaFLVGQMFsfQPRRHWTtQDCNCSIYAGHi

SEQ ID NO: Isolate

94 27

93 26

93-94 consensus (26)

123 TGHRMAWDMMTNWSPTTTTLVLAQVMRIPSTLVDLLTGHHWGILIGvAYFCMQANWAKVILV  
123 TGHRMAWDMMTNWSPTTTTLILAQVMRIPSTLVDLLAGHHWGvLVGLAYFfSMQANWAKVILV  
TGHRMAWDMMTNWSPTTTTLILAQVMRIPSTLVDLLaGHHWGvLvGLAYFfSMQANWAKVILV

SEQ ID NO: Isolate

94 27

93 26

93-94 consensus (Z6)

```

184  LFLyAGVDA
      ||| ||||
184  LFLFAGVDA
      ||| ||||
      LFLfAGVDA

```

FIGURE 2G

<u>SEQ ID NO:</u>	<u>Isolate</u>	
98	SA5	1 VPYRNASGVYHVTNDCPNSSIVYEADNLILHAPGCVPCVkegNVSRCWVQITPTLSAPNLG
100	SA7	1 VPYRNASGVYHVTNDCPNSSIVYEADNLILHAPGCVPCVRQnNVSRCWVQITPTLSAPNLG
97	SA4	1 VPYRNASGVYHVTNDCPNSSIVYEADNLILHAPGCVPCVRQDNVSkCWVQITPTLSAPNLG
96	SA1	1 VPYRNASGVYHVTNDCPNSSIVYEADsLILHAPGCVPCVRQDNVSRWVQITPTLSAPtfg
99	SA6	1 VPYRNASGVYHVTNDCPNSSIVYEADDLILHAPGCVPCVRkDNVSRWVhITPTLSAPSLG
101	SA13	1 VPYRNASGVYHVTNDCPNSSIVYEADDLILHAPGCVPCVRqgNVSRCWVqITPTLSAPSLG
96-101	consensus	VPYRNASGVYHVTNDCPNSSIVYEADnLILHAPGCVPCVrqdNVsrCWVqITPTLSAPnlG

<u>SEQ ID NO:</u>	<u>Isolate</u>	
98	SA5	62 AVTAPLRRvVDYLAGGAALCSALYVGDACGAVFLVGQMFtYRPRQHTTVQDCNCISIYSGHI
100	SA7	62 AVTAPLRRvVDYLAGGAALCSALYVGDACGAVFLVGQMFsYRPRQHTTVQDCNCISIYSGHI
97	SA4	62 AVTAPLRRvVDYLAGGAALCSALYVGDACGAVFLVGQMFtYRPRQHTTVQDCNCISIYSGHI
96	SA1	62 AVTAPLRRvVDYLAGGAALCSALYVGDACGAVFLVGQMFtYRPRQHTTVQDCNCISIYSGHI
99	SA6	62 AVTAPLRRvVDYLAGGAALCSALYVGdvCGAlFLVGQMFtYRPRQHaTVQDCNCISIYSGHI
101	SA13	62 AVTAPLRRvVDYLAGGAALCSALYVGDaCGAvFLVGQMFtYsPRrHnvVQDCNCISIYSGHI
96-101	consensus	AVTAPLRRaVDYLAGGAALCSALYVGDaCGAvFLVGQMFtYrPRqHttVQDCNCISIYSGHI

<u>SEQ ID NO:</u>	<u>Isolate</u>	
98	SA5	123 TGHMAWDMMMNWSPTTALVMAQvLRIPQVVIDIIAGGHWGVLFAvAYFASAANWAKVVLV
100	SA7	123 TGHMAWDMMMNWSPTTALVMAQLLRIPQVVIDIIAGGHWGVLFAAAyFASAANWAKVVLV
97	SA4	123 TGHMAWDMMMNWSPTTALLMAQLLRIPQVVIDIIAGGHWGVLFAAAyFASAANWAKViLV
96	SA1	123 TGHMAWDMMMNWSPTTALLMAQMLRIPQVVIDIIAGGHWGVLFAAAyFASAANWAKVVLV
99	SA6	123 TGHMAWDMMMNWSPaTALVMAQMLRIPQVVIDIIAGGHWGVLFAAAyFASAANWAKVVLV
101	SA13	123 TGHMAWDMMMNWSptTALVMAQlLRIPQVVIDIIAGaHWGVLFAAAyYASAANWAKVVLV
96-101	consensus	TGHMAWDMMMNWSptTALvMAQlLRIPQVVIDIIAGgHWGVLFAaAYfASAANWAKVvLV



FIGURE 2G

<u>SEQ ID NO:</u>	<u>Isolate</u>		
98	SA5	184	LFLFAGVDg 
100	SA7	184	LFLFAGVDA 
97	SA4	184	LFLFAGVDA 
96	SA1	184	LFLFAGVDg 
99	SA6	184	LFLFAGVDA 
101	SA13	184	LFLFAGVDA 
96-101	consensus		LFLFAGVDa

09084591.0526593

FIGURE 2H

SEQ ID NO:    Genotype  
 81-84            (IV/2b)  
                   (2c)  
 77-80            (III/2a)  
 86-90            (V/3a)  
 60-76            (II/1b)  
 52-59            (I/1a)  
                   (4a)  
 93-94            (4c)  
                   (4d)  
                   (4b)  
 96-101           (5a)  
                   (6a)  
 52-102           consensus

1 VEVrNiSsSYATNDCSNnSITWQLTnAVLHLPgcVPCENDNGTLrCWIQVTPNVAVKHRC  
 1 VEVKDTGDSYMPNTNDCSNSSIVWQLEGAVLHTPGCVPCERTANVSRCWVPVAPNLAI SQPC  
 1 aqVknTstSYMTNDCSNdSITWQLqAAVLHVPgcVPCekvGntSRCWIPVsPNVAVqqPC  
 1 LEWRntSGLYvLTNDCSNSSIVYEADDVILHTPGCVPCVQDGNTStCWTPVTPTVAVRYVQ  
 1 yEVrNVSGvYhVTNDCSNsSiVyEaaDmImHTPGCVPCVrEnNsSrCWVALtPTLAARNa  
 1 yQVRNStGLYHVTNDCPNSSIVYEaADaILHsPGCVPCVREgnasrCWVavtPTVATRDGK  
 1 EHYRNASGIYHITNDCPNSSIVYEADHHILHLPgcVPCVMTGNTSRCWTPVTPTVAVAHPC  
 1 VNYrNASGVYHVTNDCPNSSIVYEAEHqILHLPgcVPCVrVnQSRCWVALTPTVAVsYIC  
 1 YNYRNSSGVYHVTNDCPNSSIVYETDYHILHLPgcVPCVREGNKSTCWVSLTPTVAAQHNL  
 1 VHYRNASGVYHVTNDCPNSSIVYETEHIMHLPgcVPCVrTENTSRCWVPLTPTVAAYPN  
 1 VPYRNASGVYHVTNDCPNSSIVYEADnLILHAPgcVPCVrqqDNVsrCWVqITPTLSAPnLG  
 1 LTYGNSSGLYHLTNDCPNSSIVLEADAMILHLPgcVPCVrVDDRSTCWHA VTPTLAIPNAS

Y T NDC N S

H PGC PC

CW

P

SEQ ID NO:    Genotype  
 81-84            (IV/2b)  
                   (2c)  
 77-80            (III/2a)  
 86-90            (V/3a)  
 60-76            (II/1b)  
 52-59            (I/1a)  
                   (4a)  
 93-94            (4c)  
                   (4d)  
                   (4b)  
 96-101           (5a)  
                   (6a)  
 52-102           consensus

62 ALTHNLRLtHvDmIVMAATVCSALYVGdVCGAVMIvSQAfIiSPeRhnFTQECNCsIYQGHl  
 62 ALTKGLRAHIDIIVMSATVCSALYVGdVCGALMLAAQVVVSPQHHTFVQECNCsIYPGRl  
 62 ALTQGLRTHIDMVMSATLCSALYVGdLcGGvMLAAQMFIVsPqhHwFVQeCNCsIYPGTI  
 62 ATTASIRSHVDLLVGAAmCSALYVGdMCGAVFLVGQAFTFRPRRHQTvQTCNCsLYPGHl  
 62 vpTttIRrHVDLLVGAAaFCSaMYVGdLcGSvFLvSQLFTfSPRrheTvQdCNCsIYPGHv  
 62 LPatQLRRhIDLLVGSATLCSALYVGdLcGSvFLvSQLFTfSPRrheTvQdCNCsIYPGHv  
 62 APLESFRRHVDLMVGAATLCSALYVGdLcGGAFLMGQMITFRPRRHWTtQdCNCsIYPGHl  
 62 APLdSlRRHVDLMVGAATVCSALYvGDLCGGAFLVGQMFsFQPRRHWTtQdCNCsIYAGHl  
 62 APLESFRRHVDLMVGAATLCSALYIGdVCGGVFLVGQLFtFQPRRHWTtQdCNCsIYTGHl  
 62 APLESFRRHVDLMVGAATMCSAFYIGdLcGGAFLVGQLFdFRPRRHWTtQdCNCsIYPGHV  
 62 AVTAPLRRaVDYLAGGAALCSALYVGdMCGAVFLVGQMFtYrPRqHttVQDCNCsIYSGHl  
 62 TPATGFRRHVDLLAGAAVVCSSLYIGdLcGSFLAGQLFtFQPRRHWTtQdCNCsIYTGHV

R D

A CS Y GD CG

Q

P

Q CNCs Y G

SEQ ID NO:    Genotype  
 81-84            (IV/2b)  
                   (2c)  
 77-80            (III/2a)  
 86-90            (V/3a)  
 60-76            (II/1b)  
 52-59            (I/1a)  
                   (4a)  
 93-94            (4c)  
                   (4d)  
                   (4b)  
 96-101           (5a)  
                   (6a)  
 52-102           consensus

123 TGHrMAWDMMLNWSPTTLTMI LAYAArVPELvLeVVFGGHWGVVFGLAYFSMQGAWAKVIAI  
 123 TGHrMAWDMMLNWSPTTTLMLAYLVRIPEVILDI VTGGHWGVMFGLAYFSMQGSWAKVIVI  
 123 TGHrMAWDMMLNWSPTaTmILAYaMRVPEVIIdIIsGAHWGVmFGLAYFSMQGAWAKVvVI  
 123 SGHrMAWDMMLNWSPAVGmVVAHVLRlPQTlFDIiAGAHWGIlAGLAYFSMQGNWAKVAIi  
 123 sGHrMAWDMMLNWSPTaALVvSQLLRiPQAvvDmVaGAHWGvLAGLAYFSMvGNWAKVLIV  
 123 TGHrMAWDMMLNWSPTtALVvAQLLRiPQAIldMIAGAHWGvLAGLAYFSMvGNWAKVLvV  
 123 TGHrMAWDMMLNWSPTTTLlLAQVMRIPTLVDLLaGGHWGvLvGLAYFSMQANWAKVILV  
 123 TGHrMAWDMMLNWSPTATLVLAQLMRI PGAMVDLLAGGHWGIlVGIAYFSMQANWAKVILV  
 123 SGHrMAWDMMLNWSPTSALIMAQILRIPIsILGDLlTGGHWGvLAGLAFFSMQSNWAKVILV  
 123 TGHrMAWDMMLNWSPTaLVMaQILRI PQVVIDI IAGqHWGVLFaaAYfASAANWAKVvLV  
 123 TGHrMAWDMMLNWSPTTTLVLSSILRVPEICASVIFGGHWGILLAVAYFGMAGNWLKVLA V

GHRMAWDMML NWSP

R P

G HWG

A

W KV

FIGURE 2H

<u>SEQ ID NO:</u>	<u>Genotype</u>		
81-84	(IV/2b)	184	LLLVAGVDA
85	(2c)	184	LLLTAGVEA
77-80	(III/2a)	184	LLLaAGVDA
86-90	(V/3a)	184	MvMFSGVDA
60-76	(II/1b)	184	mLLFAGVDG
52-59	(I/1a)	184	LLLFaGVDA
91	(4a)	184	LFLFAGVDA
93-94	(4c)	184	LFLfAGVDA
95	(4d)	184	LFLFAGVDA
92	(4b)	184	LFLFAGVEG
96-101	(5a)	184	LFLFAGVDa
102	(6a)	184	LFLFAGVEA
52-102	consensus		GV

09034691.052698

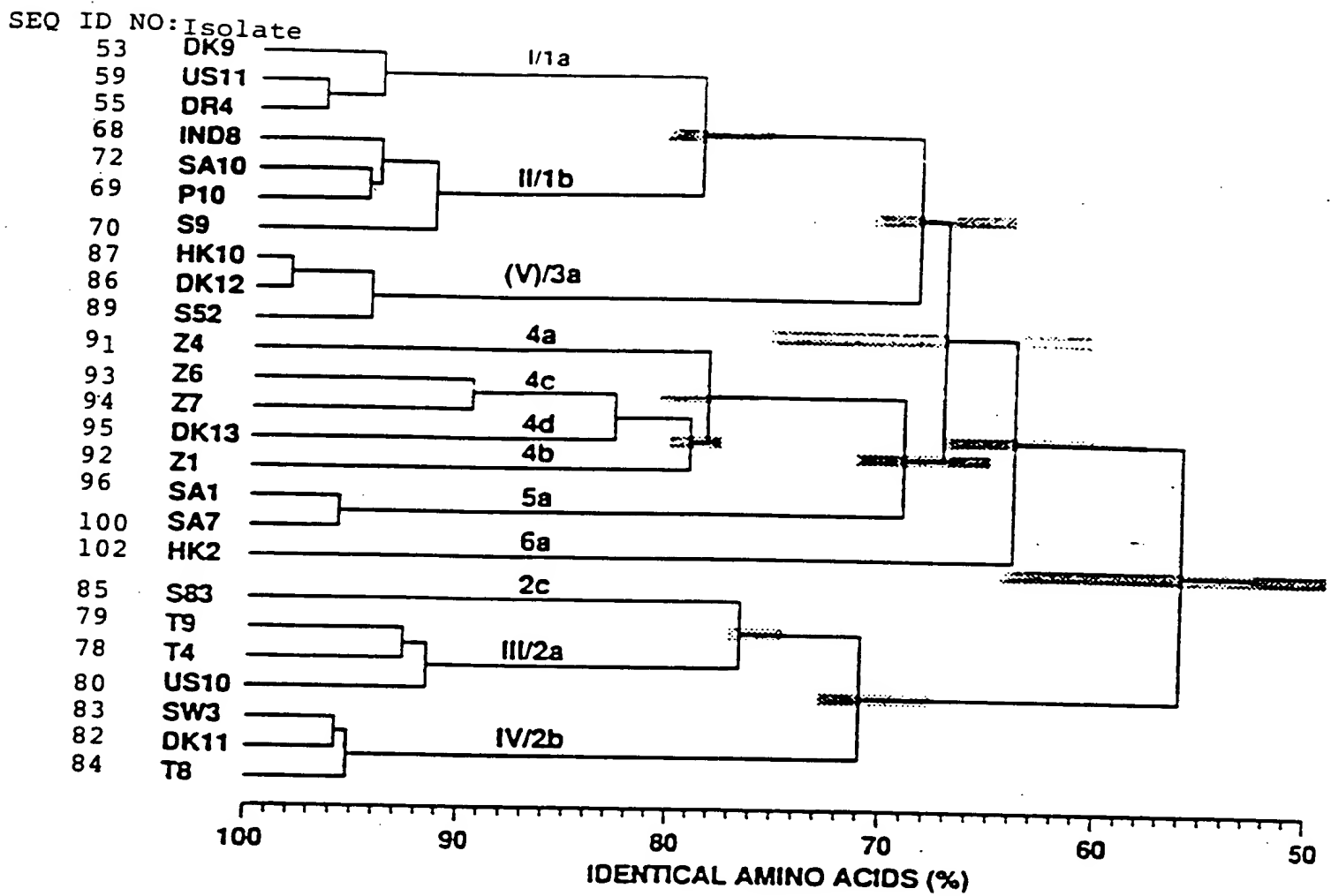
FIGURE 3

Genotype	SEQ ID NO: 52-102	Isolate	200	210	220	230	240	250	260	270	280													
			yevrnsgvYhvtNDcNs	Si	viyeaadaillHt	pgCvpc	regntsr	Cw	vavtP	tv	vaarnagap	tttLR	hvd	ll	vgaa	l	Cs	aly	v	gD	l	CG	sv	fl
IV/2b	82	DK11	VEVRNtSSS-YA	---	S-n-ITWQLTNAVL-L	---	V-ENNDGTLH	IOVT	NVAVKRGAL	THNL	AHI	MI	VMA	TV	AL	V-v	AVMIV							
	83	SW3	VEVRNtSSS-YA	---	S-b-ITWQLTNAVL-L	---	V-ENNDGTLH	IOVT	NVAVKRGAL	THNL	AHV	MI	VMA	TV	AL	V-m	AVMIV							
	81	DK8	VEVRNtSSS-YA	---	S-n-ITWQLTNAVL-L	---	V-ENNDGTLR	IOVT	NVAVKRGAL	THNL	THV	VI	VMA	TV	AL	V-v	AVMIV							
	84	T8	VEVRNtSSS-YA	---	S-n-ITWQLTNAVL-L	---	V-ENNDGTLR	IOVT	NVAVKRGAL	THNL	THV	VI	VMA	TV	AL	V-v	AVMIV							
2c	85	S83	VEVKDtGdS-Mp	---	S-b-IvwQLeqAVL-t	---	V-ETanvSR	VPVA	NIAISOPGALT	kGL	aHI	I	VMS	TV	AL	V-v	AIMLA							
III/2a	78	T4	aQVKNtNS-MV	---	S-D-ITWQLGAAVL-V	---	V-EKtGNtSR	IPVS	NVAVrPGALT	QGL	THI	MI	VMS	TL	AL	V-l	GvMLA							
	80	US10	aQVKNtNS-MV	---	S-D-ITWQLGAAVL-V	---	V-EKvGNtSR	IPVS	NVAVrPGALT	QGL	THI	MI	VMS	TL	AL	V-l	GvMLA							
	79	T9	aQVKNtNS-MV	---	S-D-ITWQLGAAVL-V	---	V-EKvGNtSR	IPVS	NVAVrPGALT	QGL	THI	MI	VMS	TL	AL	V-l	GvMLA							
	77	T2	aQVRNtSrg-MV	---	S-e-ITWQLGAAVL-V	---	V-ERlGNtSR	IPVT	NVAVrPGALT	QGL	THI	MI	VMS	TL	AL	V-l	GvMLA							
(V) /3a	86	DK12	LEVRNtSGL-VL	---	S-S-IVYEADDDVIL-T	---	V-VODGNtST	TSVT	TVAVRVVGATTASI	SHV	LL	VGA	TM	AL	V-v	AVFLV								
	87	HK10	LEVRNtSGL-VL	---	S-S-IVYEADDDVIL-T	---	V-VODGNtST	TSVT	TVAVRVVGATTASI	SHV	LL	VGA	TM	AL	V-v	AVFLV								
	88	S2	LEVRNtSGL-VL	---	S-S-IVYEADDDVIL-T	---	V-VODGNtST	TSVT	TVAVRVVGATTASI	SHV	LL	VGA	TM	AL	V-v	AVFLV								
	90	S54	LEVRNtSGL-VL	---	S-S-IVYEADDDVIL-T	---	V-VODGNtST	TSVT	TVAVRVVGATTASI	SHV	LL	VGA	TM	AL	V-v	AVFLV								
	89	S52	LEVRNtSGL-VL	---	S-S-IVYEADDDVIL-T	---	V-VODGNtST	TSVT	TVAVRVVGATTASI	SHV	LL	VGA	TM	AL	V-v	AVFLV								
	68	IND8	YEVRNtSGV-HV	---	S-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	67	IND5	YEVRNtSGV-HV	---	S-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	73	SW2	YEVRNtSGV-HV	---	S-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	63	HK3	YEVRNtSGI-HV	---	S-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	66	HK8	YEVRNtSGI-HV	---	S-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	71	S45	YEVRNtSGa-HV	---	S-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	61	D3	YEVRNtSGV-QV	---	S-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	74	T3	YEVRNtSGV-QV	---	S-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	65	HK5	YEVRNtSGV-HV	---	S-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	64	HK4	YEVRNtSGI-HV	---	S-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	76	US6	YEVRNtSGM-HV	---	S-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	69	P10	YEVRNtSGV-HV	---	S-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	72	SA10	YEVRNtSGM-HV	---	S-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	75	T10	YEVRNtSGM-HV	---	S-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	62	DK1	YEVRNtSGV-HV	---	S-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	70	S9	YEVRNtSGa-HV	---	S-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	60	D1	YEVRNtSGV-HV	---	S-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	52	DK7	YQVRNtSGL-HV	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	59	US11	YQVRNtSGL-HV	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	55	DR4	YQVRNtSGL-HV	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	54	DR1	YQVRNtSGL-HV	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	53	DK9	YQVRNtSGL-HV	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	58	SW1	YQVRNtSGL-HV	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	56	S14	YQVRNtSGL-HV	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	57	S18	YQVRNtSGL-HV	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	91	Z4	ehYRNtSGI-Hi	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	93	Z6	VNYRNtSGV-HV	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
4c	94	Z7	VNYRNtSGV-Hi	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
4d	95	DK13	VNYRNtSGV-HV	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
4b	92	Z1	VNYRNtSGV-HV	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	98	SA5	VNYRNtSGV-HV	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	100	SA7	VNYRNtSGV-HV	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	97	SA4	VNYRNtSGV-HV	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	96	SA1	VNYRNtSGV-HV	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
5a	99	SA6	VNYRNtSGV-HV	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	99	SA6	VNYRNtSGV-HV	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	101	SA13	VNYRNtSGV-HV	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								
	102	HK2	1tygNtSGI-H1	---	P-S-IVYEADADMIM-T	---	V-VREGNfS8	VALT	TLAARNASVPTTTI	rHV	LL	VGA	AP	AM	V-l	SVFLV								

FIGURE 3

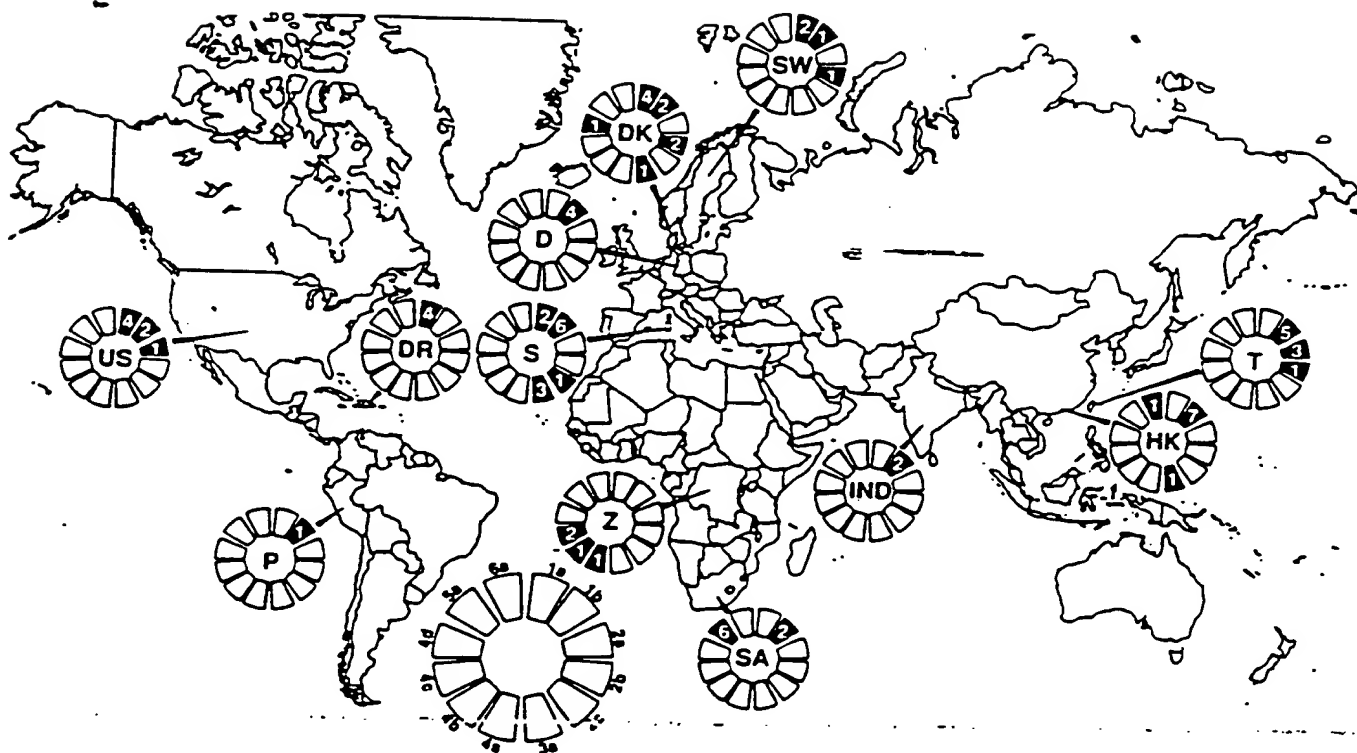
Genotype	SEQ ID NO: 52-102	Isolate	290	300	310	320	330	340	350	360	370	380	
IV/2b	82	DK11	S-AFIYS-ERHhFT-E	I-Q-HIT	L	TLTMIAYAA-V-ELVLEVF-G	VFGL-YFSMOGA-A	IAILLVA--DA					
	83	SW3	S-AFIIS-ERHhFT-E	I-Q-HIT	L	TLTMIAYAA-V-ELVLEVF-G	VFGL-YFSMOGA-A	IAILLVA--DA					
	81	DK8	S-AFIIS-ERHhFT-E	I-Q-HIT	L	TLTMIAYAA-V-ELVLEVF-G	VFGL-YFSMOGA-A	IAILLVA--DA					
	84	T8	S-AFIIS-ERHhFT-E	I-Q-HIT	L	TLTMIAYAA-V-ELVLEVF-G	VFGL-YFSMOGA-A	IAILLVA--DA					
2c	85	S83	A-VVVS-QHhFT-E	I-P-HIT	M	TTTMIAYV-i-EVILDIVT-G	VMFGL-YFSMOGA-A	IVILLTA--ea					
	78	T4	A-MFVS-QHhFT-E	I-P-HIT	M	TTTMIAYV-i-EVILDIVT-G	VMFGL-YFSMOGA-A	IVILLTA--ea					
III/2a	80	US10	A-MFVS-QHhFT-E	I-P-HIT	M	TTTMIAYV-i-EVILDIVT-G	VMFGL-YFSMOGA-A	IVILLTA--ea					
	79	T9	A-MFVS-QHhFT-E	I-P-HIT	M	TTTMIAYV-i-EVILDIVT-G	VMFGL-YFSMOGA-A	IVILLTA--ea					
	77	T2	A-MFVS-QHhFT-E	I-P-HIT	M	TTTMIAYV-i-EVILDIVT-G	VMFGL-YFSMOGA-A	IVILLTA--ea					
	86	DK12	G-AFTER-RRHhFT-E	L-P-HIT	M	AVGMVVAHV-L-OTLFDILA-A	IMAGL-YFSMOGA-A	AIIMMFS--DA					
(V)/3a	87	HK10	G-AFTER-RRHhFT-E	L-P-HIT	M	AVGMVVAHV-L-OTLFDILA-A	IMAGL-YFSMOGA-A	AIIMMFS--DA					
	88	S2	G-AFTER-RRHhFT-E	L-P-HIT	M	AVGMVVAHV-L-OTLFDILA-A	IMAGL-YFSMOGA-A	AIIMMFS--DA					
	90	S54	G-AFTER-RRHhFT-E	L-P-HIT	M	AVGMVVAHV-L-OTLFDILA-A	IMAGL-YFSMOGA-A	AIIMMFS--DA					
	89	S52	G-AFTER-RRHhFT-E	L-P-HIT	M	AVGMVVAHV-L-OTLFDILA-A	IMAGL-YFSMOGA-A	AIIMMFS--DA					
II/1b	68	IND8	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	67	IND5	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	73	SW2	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	63	HK3	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	66	HK8	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	71	S45	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	61	D3	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	74	T3	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	65	HK5	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	64	HK4	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	76	US6	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	69	P10	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	72	SA10	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	75	T10	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	62	DK1	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	70	S9	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
I/1a	60	D1	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	52	DK7	G-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	59	US11	G-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	55	DR4	G-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	54	DR1	G-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	53	DK9	G-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	58	SW1	G-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	56	S14	G-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	57	S18	G-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVVSOLL-I-OAVDMVA-A	ILAGL-YFSMOGA-A	LIVMLLFA--DG					
	91	Z4	G-MFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-EFIDMVA-G	VLGL-YFSMOGA-A	LIVMLLFA--DG					
	93	Z6	G-MFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-EFIDMVA-G	VLGL-YFSMOGA-A	LIVMLLFA--DG					
	94	Z7	G-MFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-EFIDMVA-G	VLGL-YFSMOGA-A	LIVMLLFA--DG					
	4d	DK13	G-LFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-EFIDMVA-G	VLGL-YFSMOGA-A	LIVMLLFA--DG					
	4b	92	Z1	G-LFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-EFIDMVA-G	VLGL-YFSMOGA-A	LIVMLLFA--DG				
		98	SA5	G-MFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-EFIDMVA-G	VLGL-YFSMOGA-A	LIVMLLFA--DG				
	5a	100	SA7	G-MFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-EFIDMVA-G	VLGL-YFSMOGA-A	LIVMLLFA--DG				
97		SA4	G-MFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-EFIDMVA-G	VLGL-YFSMOGA-A	LIVMLLFA--DG					
96		SA1	G-MFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-EFIDMVA-G	VLGL-YFSMOGA-A	LIVMLLFA--DG					
99		SA6	G-MFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-EFIDMVA-G	VLGL-YFSMOGA-A	LIVMLLFA--DG					
6a	101	SA13	G-MFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-EFIDMVA-G	VLGL-YFSMOGA-A	LIVMLLFA--DG					
	102	HK2	G-LFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-EFIDMVA-G	VLGL-YFSMOGA-A	LIVMLLFA--DG					

FIGURE 4



0503491.033 0503491.033

FIGURE 5



869250 " T6948060

FIGURE 6A

## SEQ ID NO: ISOLATE

108 DR4  
103 DK7  
104 US11  
105 S14  
106 SW1  
107 S18

103-108 consensus

1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG  
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG  
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG  
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG  
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG  
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG

ATGAGCACgAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG

## SEQ ID NO: ISOLATE

108 DR4  
103 DK7  
104 US11  
105 S14  
106 SW1  
107 S18

103-108 consensus

62 ACGTCAAGTTCCCGGGTGGCGGTGAGATCGTTGGTGGAGTTTACTTGTGTCGCGCAGGGG  
62 ACGTCAAGTTCCCGGGTGGCGGTGAGATCGTTGGTGGAGTTTACTTGTGTCGCGCAGGGG  
62 ACGTCAAGTTCCCGGGTGGCGGTGAGATCGTTGGTGGAGTTTACTTGTGTCGCGCAGGGG  
62 ACGTCAAGTTCCCGGGTGGCGGTGAGATCGTTGGTGGAGTTTACTTGTGTCGCGCAGGGG  
62 ACGTCAAGTTCCCGGGTGGCGGTGAGATCGTTGGTGGAGTTTACTTGTGTCGCGCAGGGG  
62 ACGTCAAGTTCCCGGGTGGCGGTGAGATCGTTGGTGGAGTTTACTTGTGTCGCGCAGGGG

ACGTcAAGTTCCCGGGTGGCGGTGAGATCGTTGGTGGAGTTTACTTGTGTCGCGCAGGGG

## SEQ ID NO: ISOLATE

108 DR4  
103 DK7  
104 US11  
105 S14  
106 SW1  
107 S18

103-108 consensus

123 CCCTAGATTGGGTGTGCGCGCGaCGAGGAAGACTTCCGAGCGGTGCGAACCTCGAGGTAGA  
123 CCCTAGATTGGGTGTGCGCGCGcCGAGGAAGACTTCCGAGCGGTGCGAACCTCGAGGTAGA  
123 CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTGCGAACCTCGAGGTAGA  
123 CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTGCGAACCTCGAGGTAGA  
123 CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTGCGAACCTCGAGGTAGA  
123 CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTGCGAACCTCGcGGTAGA

CCCTAGATTGGGTGTGCGCGCGaCGAGGAAGACTTCCGAGCGGTGCGAACCTCGaGGTAGA

## SEQ ID NO: ISOLATE

108 DR4  
103 DK7  
104 US11  
105 S14  
106 SW1  
107 S18

103-108 consensus

184 CGTCAGCCTATCCCCAAGGCgCGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC  
184 CGTCAGCCTATCCCCAAGGCACGTGCGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC  
184 CGTCAGCCTATCCCCAAGGCACGTGCGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC  
184 CGTCAGCCTATCCCCAAGGCACGTGCGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC  
184 CGTCAGCCTATCCCCAAGGCACGTGCGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC  
184 CGTCAGCCTATCCCCAAGGCACGTGCGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC

CGTCAGCCTATCCCCAAGGC - CGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC

## SEQ ID NO: ISOLATE

108 DR4  
103 DK7  
104 US11  
105 S14  
106 SW1  
107 S18

103-108 consensus

245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTcCCCCGTGG  
245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGG  
245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGG  
245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGG  
245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGgTGGGCGGGATGGCTCCTGTCTCCCCGTGG  
245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGgTGGGCGGGATGGCTCCTGTCTCCCCGTGG

CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGgTGGGCGGGATGGCTCCTGTCTCCCCGTGG

## SEQ ID NO: ISOLATE

108 DR4  
103 DK7  
104 US11  
105 S14  
106 SW1  
107 S18

103-108 consensus

306 CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGtAGGTGCGCGCAATTTGGGTAAgGTC  
306 CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGcAGGTGCGCGCAATTTGGGTAAaGTC  
306 CTCTCGGCCTAGCTGGGGCCCCACgGACCCCCGGCGTAGGTGCGCGCAATTTGGGTAAAGTTC  
306 CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTGCGCGCAATTTGGGTAAAGTTC  
306 CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTGCGCGCAATTTGGGTAAAGTTC  
306 CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTGCGCGCAATTTGGGTAAaGTC

CTCTcGGCCTAGCTGGGGCCCCcAcAGACCCCCGGCGtAGGTGCGCGCAATTTGGGTAAgGTC



FIGURE 6A

SEQ ID NO: ISOLATE

108 DR4  
103 DK7  
104 US11  
105 S14  
106 SW1  
107 S18

103-108 consensus

367 ATCGA~~c~~ACCCT~~c~~ACGTGCGGCTTCGCCGACCTCATGGGGTACAT~~c~~CCGCTCGTCGGCGCCC  
367 ATCGATAACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCC  
367 ATCGATAACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCC  
367 ATCGATAACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCC  
367 ATCGATAACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC  
367 ATCGATAACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC

ATCGA~~t~~ACCCT~~c~~ACGTGCGGCTTCGCCGACCTCATGGGGTACAT~~a~~CCGCTCGTCGGCGCCCSEQ ID NO: ISOLATE

108 DR4  
103 DK7  
104 US11  
105 S14  
106 SW1  
107 S18

103-108 consensus

428 C~~c~~CTTGGgGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGgGTTCTGGAAGACGGCGTGAA  
428 CTCTTGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA  
428 CTCTCGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA  
428 C~~c~~CTCGGgGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA  
428 CTCT~~t~~GGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA  
428 CTCT~~c~~GGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA

C~~t~~CT - GGaGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGgGTTCTGGAAGACGGCGTGAASEQ ID NO: ISOLATE

108 DR4  
103 DK7  
104 US11  
105 S14  
106 SW1  
107 S18

103-108 consensus

489 CTATGCAACAGGGA~~a~~CTTCCTGGTTGCTCTTTCTCTATCTTCCTTTTGGC~~t~~tTGCTCTCT  
489 CTATGCAACAGGGA~~a~~CTTCCTGGTTGCTCTTTCTCTATCTTCCTTTTGGCCCTGCTCTCT  
489 CTATGCAACAGGGA~~a~~CTTCCTGGTTGCTCTTTCTCTATCTTCCTTTCTGGCCCTGCTCTCT  
489 CTATGCAACAGGGA~~a~~CTTCCTGGTTGCTCTTTCTCTATCTTCCT~~c~~CTaGCCCTGCTTTCT  
489 CTATGCAACAGGGA~~a~~CTTCCTGGTTGCTCTTTCTCTATCTTCCTTTCTGGCCCTGCTTTCT  
489 CTATGCAACAGGGA~~a~~CTTCCTGGTTGCTCTTTCTCTATCTTCCTTTCTGGCCCTGCT~~c~~TCT

CTATGCAACAGGGA~~a~~CTTCCTGGTTGCTCTTTCTCTATCTTCCT~~t~~cTgGC~~c~~cTGCT~~c~~TCTSEQ ID NO: ISOLATE

108 DR4  
103 DK7  
104 US11  
105 S14  
106 SW1  
107 S18

103-108 consensus

550 TG~~c~~tTGACCGTGCCCGCaTCGGCC  
550 TGCCTGACCGTGCCCGCTTCGGCC  
550 TGCCTGACTGTGCCCGCTTCAGCC  
550 TGCCTGACTGTGCCCGCTTCAGCC  
550 TGCCTGACaGTGCCCGCGTCAGCC  
550 TG~~c~~tTGAC~~t~~GTGCCCGCGTCAG~~c~~t

TG~~c~~cTGAC~~t~~GTGCCCG~~c~~tTCaGCC

FIGURE 6B

SEQ ID NO: ISOLATE

119	S9	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
117	IND3	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
118	IND8	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
111	D1	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
112	US6	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
113	P10	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
114	DK1	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
115	T10	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
116	SW2	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
122	HK4	1	ATGAGCACGAATCCTAAACCTCAAAGAAAgACCAAACGTAACACCAACCGCCGCCACAGG
109	SA10	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
110	S45	1	ATGAGCACGAATCCTAAACCTCAAAGAcAAACCAAACGTAACACCAACCGCCGCCACAGG
123	P8	1	ATGAGCACGAaTCCTAAACCTCAAAGAAAAACCAAACGTAACACCAgCCGCCGCCACAGG
124	T3	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
120	HK3	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
121	HK5	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
109-124 consensus			ATGAGCACGAaTCCTAAACCTCAAAGAAaAaACCAAACGTAACACCAaCCGCCGCCACAGG

SEQ ID NO: ISOLATE

119	S9	62	ACGTtAAGTTCCCGGGCGGTGGtCAGATCGTcGGTGGAGTTTACCTGTTGCCGCGCAGGGG
117	IND3	62	ACGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
118	IND8	62	ACGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
111	D1	62	ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
112	US6	62	ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
113	P10	62	ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
114	DK1	62	ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
115	T10	62	ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
116	SW2	62	ACGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
122	HK4	62	ACGTtAAGTTCCCGGGCGGTGGCCAGATCGTcGGTGGAGTTTACCTGTTGCCGCGCAGGGG
109	SA10	62	ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTtTaTcTGTGTCGCCGCGCAGGGG
110	S45	62	ACGTCAAGTTCCCGGGtGGcGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
123	P8	62	ACGTtAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
124	T3	62	ACGTtAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
120	HK3	62	ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
121	HK5	62	ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
109-124 consensus			ACGTcAAGTTCCCGGGcGGtGGtCAGATCGTtGGTGGAGTtTaCCTGTTGCCGCGCAGGGG

SEQ ID NO: ISOLATE

119	S9	123	CCCCAGGTTGGGTGTGCGCGCaACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
117	IND3	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
118	IND8	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
111	D1	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
112	US6	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
113	P10	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
114	DK1	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
115	T10	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
116	SW2	123	CCCCcGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
122	HK4	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
109	SA10	123	CCCCAGGTTGGGTGTGCGCGCGAcgAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
110	S45	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcCaCAACCTCGTGGAcGG
123	P8	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGtCaTCGAACCTCGTGGcAGG
124	T3	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
120	HK3	123	CCCCAGGTTGGGTGTGCGCGCGcGACcAGGAAGACTTcAGAGCGGTcGCAACCTCGTGGAAAGG
121	HK5	123	CCCCAGGTTGGGTGTGCGCGCGACcAGGAAGACTTcGAGCGGTcGCAACCTCGTGGAAAGG
109-124 consensus			CCCCaGGTTGGGTGTGCGCGcGAcTAgGAAGACTTcGAGCGgTCgCAACCTCGTGGaaGG

SEQ ID NO: ISOLATE

119	S9	184	CGACAACCTATCCCCAAGGCTCGCCatCCCGAGGGcAGGGCCTGGGCTCAGCCCGGGTACC
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FIGURE 6B

117	IND3	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTTGGGCTCAGCCCGGGTACC
118	IND8	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTTGGGCTCAGCCCGGGcACC
111	D1	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTTGGGCTCAGCCCGGGTACC
112	US6	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC
113	P10	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC
114	DK1	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC
115	T10	184	CGACA <sub>g</sub> CCTATCCCCAAGGCTCGCCAGCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC
116	SW2	184	CGACAACCTATCCCCAAGGCTCGCCAGCCCGAGGGCAGGGCCTGGGCTCAGCctGGGTACC
122	HK4	184	CGACAACCTATCCCCAAGGCTCGCCa <sub>g</sub> CCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
109	SA10	184	CGACAACCTATCCCCAAGGCTCGCCAGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
110	S45	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC
123	P8	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTTGGGCTCAGCCCGGGCACC
124	T3	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTTGGGCTCAGCCCGGGTACC
120	HK3	184	CGACAACCTATCCCCAAGGCTCGCCa <sub>g</sub> CCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
121	HK5	184	CGACAACCTATCCCCAAGGCTCGCC <sub>g</sub> ACCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC

109-124 consensus

CGACA<sub>a</sub>CCTATCCCCAAGGCTCGCC<sub>g</sub>gCCCGAGGGcAGG<sub>g</sub>CCTGGGCTCAGCCcGGGtAcC

SEQ ID NO: ISOLATE

119	S9	245	CTTGGCCCCCTCTAcGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCGtGG
117	IND3	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCGCGG
118	IND8	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCGCGG
111	D1	245	CTTGGCCCCCTCTATGGCAACGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCGCGG
112	US6	245	CTTGGCCCCCTCTATGGCAACGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCGCGG
113	P10	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCGTGG
114	DK1	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCGcGG
115	T10	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCGtGG
116	SW2	245	CcTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCGCGG
122	HK4	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCGCGG
109	SA10	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCGTGG
110	S45	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCGTGG
123	P8	245	CTTGGCCCCCTCTATGcCAATGAGGGCTTGGGGTGGGCgGGATGGCTCCTGTcACCCCGCGG
124	T3	245	CTTGGCCCCCTCTATGGCgACGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCGCGG
120	HK3	245	CTTGGCCCCCTCTATGGCAACGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCGCGG
121	HK5	245	CTTGGCCCCCTCTATGGCAAtGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCA <sub>t</sub> GG

109-124 consensus

CtTGGCCCCCTCTAtGgCaAtGAGGGC - TGGG<sub>g</sub>TGGGCaGGATGGCTCCTGTcACCCGcGG

SEQ ID NO: ISOLATE

119	S9	306	cTCTCGGCCTAGTTGGGGCCCCAatGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
117	IND3	306	tTCTCGGCCTAGTTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
118	IND8	306	CTCTCGGCCTAGTTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
111	D1	306	CTCCCGGCCTAGTTGGGGCCCCACcGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
112	US6	306	CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
113	P10	306	CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
114	DK1	306	CTCTCGGCCTAGTTGGGGCCCCAa <sub>c</sub> GACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
115	T10	306	CTCcGGCCTAGTTGGGGCCCCACaGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
116	SW2	306	CTCTCGGCCTAGTTGGGGCCCCACtGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
122	HK4	306	CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGcAATTTGGGTAAGGTC
109	SA10	306	CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGtAATTTGGGTAAGGTC
110	S45	306	CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
123	P8	306	CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
124	T3	306	CTCCCGGCCTAATTTGGGGCCCCACaGACCCCCGGCGTAGGTCGCGtAATtTGGGTAAGGTC
120	HK3	306	CTCTCGGCCTAATTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGcAATTTGGGTAAGGTC
121	HK5	306	CTCTCGGCCTAgTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGtAATTTGGGTAAGGTC

109-124 consensus

cTCTCGGCCTAgTTGGGGCCCCAcgGACCCCCGGCGTAGGTCGCGtAATtTGGGTAAGGTC

SEQ ID NO: ISOLATE

119	S9	367	ATCGATACCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCC
117	IND3	367	ATCGATACCCTCACATGCGGCTTcGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC
118	IND8	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC

FIGURE 6B

111	D1	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC
112	US6	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
113	P10	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
114	DK1	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
115	T10	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
116	SW2	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
122	HK4	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
109	SA10	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
110	S45	367	ATCGATAACCCTCACgTGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
123	P8	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGgCC
124	T3	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCtC
120	HK3	367	ATCGATAACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGtGCC
121	HK5	367	ATCGATAACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGcGCC
109-124 consensus			ATCGATAACCCTCACaTGCGGCTTCGCCGACCTCATGGGGTACATtCCGCTCGTCGGcGccC

SEQ ID NO:	ISOLATE	
119	S9	428 CCCTAGGGGGCGCTGCCAGGGCtCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
117	IND3	428 CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
118	IND8	428 CCCTAGGGGGTGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
111	D1	428 CCCTAGGGGGTGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
112	US6	428 CCCTAGGGGGCGCTGCCAGGGCCtTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
113	P10	428 CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
114	DK1	428 CCCTAGGGGGCGCTGCCAGGGCCtTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
115	T10	428 CCCTAGGGGGCGCTGCCAGGGCtCTGGCaCATGGtGTCCGGGTtCTGGAGGACGGCGTGAA
116	SW2	428 CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
122	HK4	428 CCTTAGGGGGCGtTGCCAGaGCCCTGGCaCATGGtGTCCGGGTtTgTGGAGGACGGCGTGAA
109	SA10	428 CtTTAGGGGGCGCTGCCAGgGCCTTGGCGCATGGCGTCCGGGTtCTGGAaGACGGCGTGAA
110	S45	428 CCCTAGGGGGCGCTGCCAGaGCCTTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
123	P8	428 CCCTAGGGGGCGTTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtTgTGGAGGACGGCGTGAA
124	T3	428 CctTAGGGGGCGTTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
120	HK3	428 CCCTAGGGGGCGTTGCCAGAGCCtTGGCACATGGTGTCCGGGTtCTGGAGGACGGCGTGAA
121	HK5	428 CCCTAGGGGGCGTTGCCAGAGCCcTGGCACAcGGTGTCCGGGTtCTGGAGGACGGCGTGAA
109-124 consensus		CccTAGGGGGcGcTGCCAGgGCcctTGGCGcATGGcGTCCGGGTtctTGGAgGACGGCGTGAA

SEQ ID NO:	ISOLATE	
119	S9	489 CTATGCAACAGGGAACcTcCCCCGGTTGCTCTTTCTCTATCTTCCTTctgGCTTTGCTgTCC
117	IND3	489 CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTaGCTTTGCTATCC
118	IND8	489 CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTGGCTTTGCTATCC
111	D1	489 tTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC
112	US6	489 CTATGCAACAGGGAACtTGCCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC
113	P10	489 CTATGCAACAGGGAATcTGCCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC
114	DK1	489 CTAcGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTCTGtTGTCC
115	T10	489 CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTCTGCTGTCC
116	SW2	489 CTATGCAACAGGGAATcTGCCCCGGTTGCTcCTTTCTATCTTCCTCTTGGCTtTGCTGTCC
122	HK4	489 CTATGCAACAGGGAATTTGCCCGGTTGCTcCTTTCTATCTTCCTCTTGGCTtTGCTGTCC
109	SA10	489 CTATGCAACAGGGAATTTGCCCGGTTGCGcCTTTCTCTATCTTCCTCTTGGCTtTGCTGTCC
110	S45	489 CTATGCAACAGGGAATCTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTcTGCTGTCC
123	P8	489 CTATGCAACAGGGAATCTGCTGTTGCTCTTTCTCTATCTTCCTCTTGGCTtTGCTGTCC
124	T3	489 tTAcGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC
120	HK3	489 CTAtGCAACAGGGAATTaTACCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC
121	HK5	489 CTAcGCAACAGGGAATaTACCCGGTTGCTCTTTCTCTATCTTCCTtTTGGCTTTGCTGTCC
109-124 consensus		cTAtGCAACAGGGAAttTgCCcGGTTGCTcCtTTcTCTATCTTCCTctTgGCTtTGcTgTCC

SEQ ID NO:	ISOLATE	
119	S9	550 TGTTTGACCATCCCAGCTTCCGCT
117	IND3	550 TGTTTGACCATCCCAGCTTCCGCT
118	IND8	550 TGTTTGACCgTCCCAGCTTCCGCT
111	D1	550 TGTTTGACCATCCCAGCTTCCGCT
112	US6	550 TGTTTGACCATcCCAGCTTCCGCT

FIGURE 6B

113	P10	550	TGccTGACCATCCCAGCgTCCGCT
114	DK1	550	TGTtTGACCATCCCAGCTTCCGcc
115	T10	550	TGTCTGACCATCCCAGCTTCCGCT
116	SW2	550	TGTCTGACCATCCCAGCTTCCGCT
122	HK4	550	TGTTTGACCATCCCAGCTTCCGCT
109	SA10	550	TGTTTaACCATCCCAGCTTCCGCT
110	S45	550	TGcTTGACCATCCCAGCTTCCGCT
123	P8	550	TGtcTGACCATCCCAGCTTCCGCT
124	T3	550	TGCTTGACCATCCCAGCTTCCGCT
120	HK3	550	TGCTTGACCACCCAGCTTCCGCT
121	HK5	550	TGtcTGACCACCCAGtTCCGCT
109-124	consensus		TGttTgACCatcCCAGctTCCGct

09024591.052693  
069250" T6942060

FIGURE 6C

SEQ ID NO: ISOLATE

119	S9	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
117	IND3	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
118	IND8	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
111	D1	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
112	US6	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
113	P10	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
114	DK1	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
115	T10	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
116	SW2	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
122	HK4	1	ATGAGCACGAATCCTAAACCTCAAAGAAAGACCAAACGTAACACCAACCGCCGCCACAGG
109	SA10	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
110	S45	1	ATGAGCACGAATCCTAAACCTCAAAGAAcAAACCAAACGTAACACCAACCGCCGCCACAGG
123	P8	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAAGcCGCCGCCACAGG
124	T3	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
120	HK3	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
121	HK5	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
108	DR4	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG
104	US11	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG
105	S14	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG
106	SW1	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG
107	S18	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG
103	DK7	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG

103-124 consensus

ATGAGCACGAATCCTAAACCTCAAAGAAaAACCAAACGTAACACCAaCCGcCGCCGCCACAGG

SEQ ID NO: ISOLATE

119	S9	62	ACGTcAAGTTCCCGGGCGGTGGTcCAGATCGTcGGTGGAGTTTACCTGTTGCCGCGCAGGGG
117	IND3	62	ACGTcAAGTTCCCGGGCGGTGGTcCAGATCGTtGGTGGAGTTTACCTGTTGCCGCGCAGGGG
118	IND8	62	ACGTcAAGTTCCCGGGCGGTGGTcCAGATCGTtGGTGGAGTTTACCTGTTGCCGCGCAGGGG
111	D1	62	ACGTcAAGTTCCCGGGCGGTGGTcCAGATCGTtGGTGGAGTTTACCTGTTGCCGCGCAGGGG
112	US6	62	ACGTcAAGTTCCCGGGCGGTGGTcCAGATCGTtGGTGGAGTTTACCTGTTGCCGCGCAGGGG
113	P10	62	ACGTcAAGTTCCCGGGCGGTGGTcCAGATCGTtGGTGGAGTTTACCTGTTGCCGCGCAGGGG
114	DK1	62	ACGTcAAGTTCCCGGGCGGTGGTcCAGATCGTtGGTGGAGTTTACCTGTTGCCGCGCAGGGG
115	T10	62	ACGTcAAGTTCCCGGGCGGTGGTcCAGATCGTtGGTGGAGTTTACCTGTTGCCGCGCAGGGG
116	SW2	62	ACGTcAAGTTCCCGGGCGGTGGTcCAGATCGTtGGTGGAGTTTACCTGTTGCCGCGCAGGGG
122	HK4	62	ACGTcAAGTTCCCGGGCGGTGGTcCAGATCGTtGGTGGAGTTTACCTGTTGCCGCGCAGGGG
109	SA10	62	ACGTcAAGTTCCCGGGCGGTGGTcCAGATCGTtGGTGGAGTTTACCTGTTGCCGCGCAGGGG
110	S45	62	ACGTcAAGTTCCCGGGcGGcGGTcCAGATCGTtGGTGGAGTTTACCTGTTGCCGCGCAGGGG
123	P8	62	ACGTtAAGTTCCCGGGCGGTGGTcCAGATCGTtGGTGGAGTTTACCTGTTGCCGCGCAGGGG
124	T3	62	ACGTtAAGTTCCCGGGCGGTGGTcCAGATCGTtGGTGGAGTTTACCTGTTGCCGCGCAGGGG
120	HK3	62	ACGTtAAGTTCCCGGGCGGTGGTcCAGATCGTtGGTGGAGTTTACCTGTTGCCGCGCAGGGG
121	HK5	62	ACGTcAAGTTCCCGGGCGGTGGTcCAGATCGTtGGTGGAGTTTACCTGTTGCCGCGCAGGGG
108	DR4	62	ACGTcAAGTTCCCGGGTGGCGGTcCAGATCGTtGGTGGAGTTTACTTGTtGCCGCGCAGGGG
104	US11	62	ACGTcAAGTTCCCGGGTGGCGGTcCAGATCGTtGGTGGAGTTTACTTGTtGCCGCGCAGGGG
105	S14	62	ACGTcAAGTTCCCGGGTGGCGGTcCAGATCGTtGGTGGAGTTTACTTGTtGCCGCGCAGGGG
106	SW1	62	ACGTcAAGTTCCCGGGTGGCGGTcCAGATCGTtGGTGGAGTTTACTTGTtGCCGCGCAGGGG
107	S18	62	ACGTcAAGTTCCCGGGTGGCGGTcCAGATCGTtGGTGGAGTTTACTTGTtGCCGCGCAGGGG
103	DK7	62	ACGTcAAGTTCCCGGGTGGCGGTcCAGATCGTtGGTGGAGTTTACTTGTtGCCGCGCAGGGG

103-124 consensus

ACGTcAAGTTCCCGGGcGGtGGtCAGATCGTtGGTGGAGTtTAcCTGTTGCCGCGCAGGGG

SEQ ID NO: ISOLATE

119	S9	123	CCCCAGGTTGGGTGTGCGCGCAACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAAGG
117	IND3	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAAGG
118	IND8	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAAGG
111	D1	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAAGG
112	US6	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAAGG
113	P10	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAAGG
114	DK1	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAAGG
115	T10	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAAGG
116	SW2	123	CCCCcGGTtGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAAGG
122	HK4	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAAGG

FIGURE 6C

109	SA10	123	CCCCAGGTTGGGTGTGCGCGCgAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
110	S45	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcCaCAACCTCGTGGAAcGG
123	P8	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGaTCGCAACCTCGTGGcAGG
124	T3	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
120	HK3	123	CCCCAGGTTGGGTGTGCGCGCGACcAGGAAGACTTcAGAGCGGTcGCAACCTCGTGGAAAGG
121	HK5	123	CCCCAGGTTGGGTGTGCGCGCGACcAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
108	DR4	123	CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTcGCAACCTCGAGGTAGA
104	US11	123	CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTcGCAACCTCGAGGTAGA
105	S14	123	CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTcGCAACCTCGAGGTAGA
106	SW1	123	CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTcGCAACCTCGAGGTAGA
107	S18	123	CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTcGCAACCTCGcGGTAGA
103	DK7	123	CCCTAGATTGGGTGTGCGCGCGcCGAGGAAGACTTCCGAGCGGTcGCAACCTCGaGGTAGA

103-124 consensus

CCCcAGgTTGGGTGTGCGCGCgaCtAGGAAGACTTCCGAGCGgTCgCAACCTCGtGGAAgG

SEQ ID NO: ISOLATE

119	S9	184	CGACAACCTATCCCCAAGGCTCGCCatCCCGAGGGcAGGGCCTGGGCTCAGCCCGGGTACC
117	IND3	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
118	IND8	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGcACC
111	D1	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
112	US6	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
113	P10	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
114	DK1	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
115	T10	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
116	SW2	184	CGACAACCTATCCCCAAGGCTCGCCAGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
122	HK4	184	CGACAACCTATCCCCAAGGCTCGCCAGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
109	SA10	184	CGACAACCTATCCCCAAGGCTCGCCAGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
110	S45	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
123	P8	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGcAtC
124	T3	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
120	HK3	184	CGACAACCTATCCCCAAGGCTCGCCaACCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
121	HK5	184	CGACAACCTATCCCCAAGGCTCGCCAGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
108	DR4	184	CGTcAGCCTATCCCCAAGGCACGTcCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
104	US11	184	CGTcAGCCTATCCCCAAGGCACGTcCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
105	S14	184	CGTcAGCCTATCCCCAAGGCACGTcCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
106	SW1	184	CGTcAGCCTATCCCCAAGGCACGTcCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
107	S18	184	CGTcAGCCTATCCCCAAGGCACGTcCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
103	DK7	184	CGTcAGCCTATCCCCAAGGCcAGTcCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC

103-124 consensus

CGaCAaCCTATCCCCAAGGCTcCGcCgGcCCGAGGGcAGGgCCTGGGCTcCAGCCcGGGtAcc

SEQ ID NO: ISOLATE

119	S9	245	CTTGGCCCCCTCTAcGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGtGG
117	IND3	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
118	IND8	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
111	D1	245	CTTGGCCCCCTCTATGGCAACGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
112	US6	245	CTTGGCCCCCTCTATGGCAACGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
113	P10	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
114	DK1	245	CTTGGCCCCCTCTATGGCAATGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
115	T10	245	CTTGGCCCCCTCTATGGCAATGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
116	SW2	245	CTTGGCCCCCTCTATGGCAATGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
122	HK4	245	CTTGGCCCCCTCTATGGCAATGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
109	SA10	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
110	S45	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
123	P8	245	CTTGGCCCCCTCTATGcCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
124	T3	245	CTTGGCCCCCTCTATGGCAACGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
120	HK3	245	CTTGGCCCCCTCTATGGCAATGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
121	HK5	245	CTTGGCCCCCTCTATGGCAATGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
108	DR4	245	CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
104	US11	245	CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
105	S14	245	CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
106	SW1	245	CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGaTGGGCAGGATGGCTCCTGTcACCCCCGCGG
107	S18	245	CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG

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245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGG  
CtTGGCCCCCTCTAtGgCaAtGAGGGCttgGGgTGGGCaGGATGGCTCCTGTCTCaCCCCgtGG

306 CTCTCGGCCTAGTTGGGGCCCCAatGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC  
306 tTCTCGGCCTAGTTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC  
306 CTCTCGGCCTAGTTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC  
306 CTCCCGGCCTAGTTGGGGCCCCACcGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC  
306 CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC  
306 CTCTCGGCCTAGTTGGGGCCCCACGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC  
306 CTCTCGGCCTAGTTGGGGCCCCAacGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC  
306 CTCcCGGCCTAGTTGGGGCCCCACaGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC  
306 CTCTCGGCCTAGTTGGGGCCCCACtGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC  
306 CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGcAATTTGGGTAAGGTC  
306 CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC  
306 CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC  
306 CTCCCGGCCTAATTGGGGCCCCACaGACCCCCGGCGTAGGTCGCGcAATcTGGGTAAGGTC  
306 CTCTCGGCCTAATTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGcAATTTGGGTAAGGTC  
306 CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGcAATTTGGGTAAGGTC  
306 CTCTCGGCCTAGCTGGGGCCCCACaGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC  
306 CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC  
306 CTCcCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGcAAAGTC  
306 CTCtCGGCCTAGCTGGGGCCCCaACAGACCCCCGGCGcAGGTCGCGCAATTTGGGTAAGGTC

CTCtCGGCCTAgTtTGGGGCCCcAc-GACCCCCGGCGtAGGTCGCGtAATtTGGGtAAgGTC

[illegible]

ATCGA<sup>+</sup>ACCCT<sup>-</sup>cAc<sup>+</sup>TGCGGCTT<sup>-</sup>cGCCGACCTCATGGGGTACAT<sup>-</sup>tCCGCTCGTCGG<sup>-</sup>cG<sup>+</sup>ccc

428 CCCTAGGGGGCGCTGCCAGGGCtCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA  
428 CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTGGAGGACGGCGTGAA  
428 CCCTAGGGGGGCTGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTGGAGGACGGCGTGAA  
428 CCCTAGGGGGTGTCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA  
428 CCCTAGGGGGCGCTGCCAGGGCCtTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA



FIGURE 6C

113	P10	428	CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
114	DK1	428	CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
115	T10	428	CCCTAGGGGGCGCTGCCAGGGCtCTGGCaCATGGtGTCCGGGTTCTGGAGGACGGCGTGAA
116	SW2	428	CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGcGTCCGGGTTCTGGAGGACGGCGTGAA
122	HK4	428	CCTTAGGGGGCGtTGCCAGaGCCCTGGCaCATGGtGTCCGGGTTgTGGAGGACGGCGTGAA
109	SA10	428	CtTTAGGGGGCGCTGCCAGgGCCTTGGCGCATGGCGTCCGGGTTCTGGAAgACGGCGTGAA
110	S45	428	CCCTAGGGGGCGCTGCCAGaGCCTTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
123	P8	428	CCCTAGGGGGCGTTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTgTGGAGGACGGCGTGAA
124	T3	428	CctTAGGGGGCGTTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
120	HK3	428	CCCTAGGGGGCGTTGCCAGAGCctTGGCACATGGTGTCCGGGTTCTGGAGGACGGCGTGAA
121	HK5	428	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACaGGTGTCCGGGTTCTGGAGGACGGCGTGAA
108	DR4	428	CCCTtGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGaGTTCTGGAAAGACGGCGTGAA
104	US11	428	CtCTCGGaGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAAGACGGCGTGAA
105	S14	428	CcCTCGGgGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAAGACGGCGTGAA
106	SW1	428	CTCTtGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAAGACGGCGTGAA
107	S18	428	CTCTcGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAAGACGGCGTGAA
103	DK7	428	CTCTtGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAAGACGGCGTGAA

103-124 consensus CccTaGGgGGcGcTGCCAGgGCcctTGGCGcATGGcGTCCGgGTtctTGGAgGACGGCGTGAA

SEO ID NO:	ISOLATE	
119	S9	489 CTATGCAACAGGGAACcTcCCCCGGTTGCTCTTTCTCTATCTTCCTTcTgGCTTTGCTgTCC
117	IND3	489 CTATGCAACAGGGAACCTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTaGCTTTGCTATCC
118	IND8	489 CTATGCAACAGGGAACtTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTGCGCTTTGCTATCC
111	D1	489 tTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGCTTTGCTGTCC
112	US6	489 CTATGCAACAGGGAACtTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGCTTTGCTGTCC
113	P10	489 CTATGCAACAGGGAATcTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGCTTTGCTGTCC
114	DK1	489 CTAcGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGCTTTGCTGTCC
115	T10	489 CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGCTCTGtTGTC
116	SW2	489 CTATGCAACAGGGAATcTGCCCGGTTGCTCctTTTTCTATCTTCCTCTTGCTtTGCTGTCC
122	HK4	489 CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGCTcTGCTGTCC
109	SA10	489 CTATGCAACAGGGAATTTGCCCGGTTGcCCTTTCTCTATCTTCCTCTTGCTcTGCTGTCC
110	S45	489 CTATGCAACAGGGAATCTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGCTcTGCTGTCC
123	P8	489 CTATGCAACAGGGAATCTGCCTGGTTGCTCTTTCTCTATCTTCCTCTTGCTcTGCTGTCC
124	T3	489 tTAcGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTATCTTCCTCTTGCTTTGCTGTCC
120	HK3	489 CTAtGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTGCTTTGCTGTCC
121	HK5	489 CTAcGCAACAGGGAATaTACCCGGTTGCTCTTTCTCTATCTTCCTTTTGCTTTGCTGTCC
108	DR4	489 CTATGCAACAGGGAATCTTCCTGGTTGCTCTTTCTCTATCTTCCTTTTGCTTTGCTGTCT
104	US11	489 CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTcCTaGCCCTGCTTTCT
105	S14	489 CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTcCTaGCCCTGCTTTCT
106	SW1	489 CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTCTTGCCCTGCTTTCT
107	S18	489 CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTCTTGCCCTGCTCTCT
103	DK7	489 CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTtTGCCCTGCTCTCT

103-124 consensus cTAtGCAACAGGGAAtcTgCCcGGTTGCTCtTtCTCTATCTTCCTcTgGCTtTGcTgTCC

SEO ID NO:	ISOLATE	
119	S9	550 TGTTTGACCATCCCAGCTTCCGCT
117	IND3	550 TGTTTGACCATCCCAGCTTCCGCT
118	IND8	550 TGTTTGACCGtCCCAGCTTCCGCT
111	D1	550 TGTTTGACCATCCCAGCTTCCGCT
112	US6	550 TGTTTGACCATcCCAGCTTCCGCT
113	P10	550 TGccTGACCATCCCAGCGTCCGCT
114	DK1	550 TGTtTGACCATCCCAGCTTCCGc
115	T10	550 TGTCTGACCATCCCAGCTTCCGCT
116	SW2	550 TGTCTGACCATCCCAGCTTCCGCT
122	HK4	550 TGTTTGACCATCCCAGCTTCCGCT
109	SA10	550 TGTTTaACCATCCCAGCTTCCGCT
110	S45	550 TGcTTGACCATCCCAGCTTCCGCT
123	P8	550 TGtCTGACCATCCCAGCTTCCGCT
124	T3	550 TGCTTGACCATCCCAGCTTCCGCT
120	HK3	550 TGCTTGACCAcCCCAGCTTCCGCT
121	HK5	550 TGtCTGACCAcCCCAGcTTCCGCT

FIGURE 6C

108	DR4	550	TGctTGACCGTGCCCCGCaTCgGCC
104	US11	550	TGCCTGACTGTGCCCCGCTTCAGCC
105	S14	550	TGCCTGACTGTGCCCCGCTTCAGCC
106	SW1	550	TGCCTGACaGTGCCCCGCGTCAGCC
107	S18	550	TGtCTGACTGTGCCCCGCGTCAGCt
103	DK7	550	TGcCTGACcGTGCCCCGctTCgGCc
103-124	consensus		TGttTgACcatcCCaGctTCcGct

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369250" 16948060

FIGURE 6D

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	1 ATGAGCACAAATTCCTAAACCTCAAAGAAAAACCAAAGAAACACtAACCGTCGCCACAAg
125	T4	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACcAACCGTCGCCACAgG
126	US10	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACtAACCGTCGCCACAAg
127	T9	1 ATGAGCACAAATCCaAAACCcCAAAGAAAAACCAaAGAAACACcAACCGTCGCCACAgG
125-128	consensus	ATGAGCACAAATCCtAAACCTCAAAGAAAAACCAaAGAAACAC - AACCGTCGCCACAG - G
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	62 ACGTTAAGTTtCCGGGCGGCGGCCAGATCGTTGGCGGAGTATACTTGtTGCCGCGCAGGGG
125	T4	62 ACGTTAAGTTtCCGGGCGGCGGCCAGATCGTTGGCGGAGTATACTTGTTGCCGCGCAGGGG
126	US10	62 ACGTTAAGTTtCCGGGCGGCGGCCAGATCGTTGGCGGAGTATACTTGTTGCCGCGCAGGGG
127	T9	62 ACGTTAAGTTtCCGGGCGGCGGCCAGATCGTTGGCGGAGTATACTTGTTGCCGCGCAGGGG
125-128	consensus	ACGTTAAGTT - CCGGGCGGCGGCCAGATCGTTGGCGGAGTATACTTGtTGCCGCGCAGGGG
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	123 CCCcAGGTTGGGTGTGCGCGGACAAGGAAGACTTCGGAGCGgTCCcAGCCtCGTGGaAGG
125	T4	123 CCCcAGGTTGGGTGTGCGCGGACAAGGAAGACTTCGGAGCGaTCCcAGCCACGTGGGAGG
126	US10	123 CCCcAGGTTGGGTGTGCGCGGACAAGGAAGACTTCGGAGCGGTCCcAGCCACGTGGGAGG
127	T9	123 CCCtAGGTTGGGTGTGCGCaGACAAGGAAGACTTCGGAGCGGTCCcAGCCACGTGGGAGG
125-128	consensus	CCCcAGGTTGGGTGTGCGCGcGACAAGGAAGACTTCGGAGCGgTCCcAGCCaCGTGGgAGG
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	184 CGCCAGCCCATCCCCtAAAGATCGGCGCTCCACTGGCAAGTCCTGGGGAAAACCAGGATAcC
125	T4	184 CGCCAGCCCATCCCCAAAGATCGGCGCTCCACTGGCAAGTCCTGGGGAAAACCAGGATAtC
126	US10	184 CGCCAGCCCATCCCCAAAGATCGGCGCcCCACTGGCAAGTCCTGGGGAAAACCAGGATACC
127	T9	184 CGCCAGCCCATCCCCAAAGATCGGCGCTCCACTGGCAAGTCCTGGGGAAAACCAGGATACC
125-128	consensus	CGCCAGCCCATCCCCcAAAGATCGGCGCTCCACTGGCAAGTCCTGGGGAAAACCAGGATAcC
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	245 CCTGGCCCCCTGTATGGGAATGAGGGgCTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
125	T4	245 CCTGGCCCCCTGTATGGGAATGAGGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
126	US10	245 CtTGGCCCCCTATATGGGAATGAGGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
127	T9	245 CcTGGCCtCTATATGGGAATGAGGGACTCGGCTGGGCgGGATGGCTCCTGTCCCCCGAGG
125-128	consensus	CcTGGCCcCT - TATGGGAATGAGGGaCTCGGCTGGGCaGGATGGCTCCTGTCCCCCGAGG
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	306 TTCtCGTCCCTCtTGGGGCCCCAATGACCCCCGGCATAGGTTCGCGCAAtGTGGGTAAaGTC
125	T4	306 TTCCCGTCCCTCtTGGGGCCCCAATGACCCCCGGCATAGGTTCGCGCAACGTGGGTAAAGTC
126	US10	306 TTCCCGTCCCTCTTGGGGCCCCAcTGAtCCCCGGCATAGGTTCGCGCAACGTGGGTAAAGTC
127	T9	306 TTCCCGTCCCTCTTGGGGCCCCAgTGAcCCCCGGCATAGGTTCGCGCAACGTGGGTAAAGTC
125-128	consensus	TTCcCGTCCCTCtTGGGGCCCCAaTGAcCCCCGGCATAGGTTCGCGCAAcGTGGGTAAgGTC
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	367 ATCGATACCCTAACGTGCgGcTTGCCGACCTCATGGGTACaTCCCGTCGTAGGCGcCC
125	T4	367 ATCGATACCCTAACGTGCAGCcTTGCCGACCTCATGGGTACgTCCCGTCGTAGGCGgCC
126	US10	367 ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGaTACATCCCGTCGTgGGCGCtC
127	T9	367 ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGgTACATCCCGTCGTaGGCGCcC
125-128	consensus	ATCGATACCCTAACGTGCgGcTTGCCGACCTCATGGGgTACaTCCCGTCGTaGGCGccc
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	428 CGcTtGGTGGtGTCGCCAGAGCTCTtGCGCATGGCGTGAGAGTCCTGGAGGACGGaGTTAA

FIGURE 6D

125 T4  
126 US10  
127 T9

125-128 consensus

428 CGtTgGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA  
428 CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGgGTCCTGGAGGACGGGGTTAA  
428 CGCTTGGTGGCGTtGCCAGAGCTCTCGCGCAcGGCGTGAGaGTCCTGGAGGACGGGGTTAA

CGcTtGGTGGcGTcGCCAGAGCTCTcGCGCAtGGCGTGAGaGTCCTGGAGGACGGgGTTAA

SEQ ID NO: ISOLATE

128 T2  
125 T4  
126 US10  
127 T9

125-128 consensus

489 TTATGCAACAGGtAACTTACCcGGTTGCTCCTTTTCTATcTTCTTGCTaGCCCTgCTGTCC  
489 TTATGCAACAGGGAACtTACCtGGTTGCTCCTTTTCTATtTTCTTGCTGGCCCTACTGTCC  
489 TTATGCAACAGGGAACtTACCcGGTTGCTCCTTTTCTATCTTCTTGCTGGCCtTACTGTCC  
489 TTATGCAACAGGGAACcTACCtGGTTGCTCtTTTTCTATCTTCTTGCTGGCCcTACTGTCC

TTATGCAACAGGgAACTTACC-GGTTGCTCtTTTTCTATcTTCTTGCTgGCCcTaCTGTCC

SEQ ID NO: ISOLATE

128 T2  
125 T4  
126 US10  
127 T9

125-128 consensus

550 TGCATCACtATTCCgGTtTCaGCT  
550 TGCATCACCAttCCAGTCTCcGCT  
550 TGCATCACCAttCCAGTCTCTGCT  
550 TGCATCACCAcTCCgGcCTCTGCT

TGCATCACcAtTCC-GtcTCTcGCT

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869250" T6948060

FIGURE 6E

SEQ ID NO: ISOLATE

131 DK11  
132 SW3  
133 DK8  
129 T8  
130 US1

129-133 consensus

1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAATACAAACCGCCGCCACAGG  
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAATACAAACCGCCGCCACAGG  
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACAAACCGCCGCCACAGG  
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACAAACCGCCGCCACAGG  
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACAAACCGCCGCCACAGG

ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACAAACCGCCGCCACAGG

SEQ ID NO: ISOLATE

131 DK11  
132 SW3  
133 DK8  
129 T8  
130 US1

129-133 consensus

62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG  
62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG  
62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG  
62 ACGTCAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG  
62 ACGTCAAGTTCCCGGGTGGCGGGtCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG

ACGTtAAGTTCCCGGGTGGCGGGcCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG

SEQ ID NO: ISOLATE

131 DK11  
132 SW3  
133 DK8  
129 T8  
130 US1

129-133 consensus

123 CCCcAGGTTGGGTGTGCGCaCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA  
123 CCCcAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA  
123 CCCcAGGTTGGGTGTGCGCGCGACAAGGAAGtCTTCCGAGCGATCCCAGCCGCGTGGGAGg  
123 CCCtAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA  
123 CCCcAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA

CCCcAGGTTGGGTGTGCGCgCGACAAGGAAGaCTTCCGAGCGATCCCAGCCGCGTGGGAGa

SEQ ID NO: ISOLATE

131 DK11  
132 SW3  
133 DK8  
129 T8  
130 US1

129-133 consensus

184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGcCCTGGGGAAAGCCAGGATATC  
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGGAAAGCCAGGATATC  
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGGAAAGCCAGGATATC  
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGGAAAGCCAGGATATC  
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGGAAAgCCAGGATATC

CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGtCCTGGGGAAAgCCaGGATATC

SEQ ID NO: ISOLATE

131 DK11  
132 SW3  
133 DK8  
129 T8  
130 US1

129-133 consensus

245 CTTGGCCCCCTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG  
245 CTTGGCCCCCTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG  
245 CTTGGCCCCCTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG  
245 CTTGGCCTCTtTACGGAAACGAGGGCTGCGGtTGGGCAGGTTGGCTCCTGTCCCCCGCGG  
245 CTTGGCCTCTgTACGGAAACGAGGGCTGCGGcTGGGCAGGTTGGCTCCTGTCCCCCGCGG

CTTGGCCcCTgTAtGGAAACGAGGGCTGCGGcTGGGCAGGTTGGCTCCTGTCCCCCGCGG

SEQ ID NO: ISOLATE

131 DK11  
132 SW3  
133 DK8  
129 T8  
130 US1

129-133 consensus

306 GTCTCATCCTAATTGGGGCCCCACTGACCCCCGGCATAaATCACGCAATTTGGGtAAAGTC  
306 GTCTCATCCTAATTGGGGCCCCACTGACCCCCGGCATAGATCACGCAATTTGGGCAAGTC  
306 GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCATAGATCACGCAATTTGGGCAAGTC  
306 GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCATAGATCACGTAATTTGGGCAgAGTC  
306 GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCAcAGATCACGTAAcTTGGGCAagGTC

GTCTCgTCCTAcTTGGGGCCCCACTGACCCCCGGCAtAgATCACGCAAtTTGGGcAaaGTC

SEQ ID NO: ISOLATE

131 DK11  
132 SW3  
133 DK8  
129 T8

367 ATCGACACCATTACGTGTGGTtTTGCCGACCTCATGGGGTACATCCCTGTCTGtGGCGCCC  
367 ATCGACACCATTACGTGTGGTtTTGCCGACCTCATGGGGTACATCCCTGTCTGtGGCGCCC  
367 ATCGACACCATTACGTGTGGTtTTGCCGACCTCATGGGGTACATCCCTGTCTGtGGCGCCC  
367 ATCGATACCATTACaTGTGGTtTTGCCGACCTCATGGGGTACATCCCTGTCTGtGGCGCCC

FIGURE 6E

130 US1 367 ATCGATACCATTACgTGTGGTTTTGCCGACCTCATGGGGTACATCCCTGTCGTTGGCGCCC  
 129-133 consensus ATCGAcACCATTACgTGTGGTTTTGCCGACCTCATGGGGTACATCCCTGTCGTTGGCGCCC

SEQ ID NO: ISOLATE  
 131 DK11 428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA  
 132 SW3 428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA  
 133 DK8 428 CGGTtGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA  
 129 T8 428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACAcGGTGTTAGGGTCCTGGAAGACGGGATAAA  
 130 US1 428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACAcGGTGTTAGGGTCCTGGAAGACGGGATAAA  
 129-133 consensus CGGTcGGAGGCGTCGCCAGAGCTCTGGCACAcGGTGTTAGgGTCCTGGAAGACGGGATAAA

SEQ ID NO: ISOLATE  
 131 DK11 489 TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTTCTATCTTCTTACTTGCTCTTCTGTCa  
 132 SW3 489 TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTTCTATCTTCTTACTTGCTCTTCTGTcG  
 133 DK8 489 TTACGCAACAGGGAATTTGCCTGGTTGCTCTTTTTCTATCTTCTTACTTGCTCTTCTGTcG  
 129 T8 489 cTAtGCAACAGGGAATTTGCCTGGTTGCTCTTTTTCTATCTTCTTACTTGCTCTTCTGTcG  
 130 US1 489 tTAcGCAACAGGGAATcTGCCTGGTTGCTCtTTTTCTATCTTCTTaCTTGCTCTTCTGTcG  
 129-133 consensus tTAcGCAACAGGGAATcTGCCTGGTTGCTCtTTTTCTATCTTCTTaCTTGCTCTTCTGTcG

SEQ ID NO: ISOLATE  
 131 DK11 550 TGCTgCACAGTGCCAGTGTCTGCG  
 132 SW3 550 TGCTtCACAGTGCCAGTGTCTGCG  
 133 DK8 550 TGCTgCACAGTGCCAGTGTCTGCG  
 129 T8 550 TGCTtCACAGTGCCAGTGTCTGCA  
 130 US1 550 TGCgcCACgGTGCCgGTGTCTGCA  
 129-133 consensus TGct - CACaGTGCCaGTGTCTGcG

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FIGURE 6F

SEQ ID NO: ISOLATE

131 DK11  
132 SW3  
133 DK8  
129 T8C  
130 US1  
125 T4  
126 US10  
127 T9  
128 T2  
134 S83

125-134 consensus

1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAATACAAACCGCCGCCACAGG  
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAATACAAACCGCCGCCACAGG  
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACAAACCGCCGCCACAGG  
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACAAACCGCCGCCACAGG  
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACcAACCGTCGCCACAGG  
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACtAACCGTCGCCACAGG  
1 ATGAGCACAAATCCaAAACCcCAAAGAAAAACCAaAGAAACACcAACCGTCGCCACAGG  
1 ATGAGCACAAATTCCTAAACCTCAAAGAAAAACCAAAGAAACACTAACCGTCGCCACAGG  
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACTAACCGcCGCCACAGG

ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAaAGAAACACaAACCGcCGCCACAGG

SEQ ID NO: ISOLATE

131 DK11  
132 SW3  
133 DK8  
129 T8  
130 US1  
125 T4  
126 US10  
127 T9  
128 T2  
134 S83

125-134 consensus

62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG  
62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG  
62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG  
62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG  
62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTATACTTGTTGCCGCGCAGGGG  
62 ACGTTAAGTTcCCGGGCGGCGGCCAGATCGTTGGCGGAGTATACTTGTTGCCGCGCAGGGG  
62 ACGTTAAGTTcCCGGGCGGCGGCCAGATCGTTGGCGGAGTATACTTGTTGCCGCGCAGGGG  
62 ACGTTAAGTTcCCGGGCGGCGGCCAGATCGTTGGCGGAGTATACTTGCTGCCGCGCAGGGG  
62 ACGTcAAGTTcCCGGGCGGtGGCCAGATCGTTGGCGGAGTATACTTGCTGCCGCGCAGGGG

ACGTTAAGTTcCCGGG-GGcGGcCAGATCGTTGGCGGAGT-TACTTGcTGCCGCGCAGGGG

SEQ ID NO: ISOLATE

131 DK11  
132 SW3  
133 DK8  
129 T8  
130 US1  
125 T4  
126 US10  
127 T9  
128 T2  
134 S83

125-134 consensus

123 CCCAGGTTGGGTGTGCGCaCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA  
123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA  
123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGAGtCTTCCGAGCGATCCCAGCCGCGTGGGAGg  
123 CCCtAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA  
123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA  
123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCACGTGGGAGG  
123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGGTCCCAGCCACGTGGGAGG  
123 CCCtAGGTTGGGTGTGCGCaCGACAAGGAAGACTTCCGAGCGGTCCCAGCCACGTGGGAGG  
123 CCCcAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGGTCCCAGCCtCGTGGaAGG  
123 CCCgAGaTTGGGTGTGCGCGCGACgAGGAaACTTCCGaAGGTTCCCAGCCaCGTGGgAGG

CCCcAGgTTGGGTGTGCGCGCaAGGAAGaCTTCCGaAGCGaTCCCAGCCgCGTGGgAGg

SEQ ID NO: ISOLATE

131 DK11  
132 SW3  
133 DK8  
129 T8  
130 US1  
125 T4  
126 US10  
127 T9  
128 T2  
134 S83

125-134 consensus

184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGcCCTGGGGAAAGCCAGGATATC  
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGGAAAGCCAGGATATC  
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGGAAaACgGGATATC  
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGGAAaACcAGGATATC  
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACTGGCAAGTCTTGGGGAAaACcAGGATATC  
184 CGCCAGCCCATCCCGAAAGATCGGCGCcCCACTGGCAAGTCTTGGGGAAaACcAGGATACC  
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACTGGCAAGTCTTGGGGAAaACcAGGATACC  
184 CGCCAGCCCATCCCTAAAGATCGGCGCTCCACTGGCAAGTCTTGGGGAAaACcAGGATACC  
184 CGCCAGCCCATCCCTAAAGATCGGCGCaCCACTGGCAAGTCTTGGGGAAgCCAGGATACC

CGCCAGCCCATCCCGAAAGATCGGCGCTCCAC-GGCAAGTCTTGGGGAAaCCaGGATAtC

SEQ ID NO: ISOLATE

131 DK11  
132 SW3  
133 DK8  
129 T8

245 CTTGGCCCCGTGTATGGAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG  
245 CTTGGCCCCGTGTATGGAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG  
245 CTTGGCCCCGTGTATGGAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG  
245 CTTGGCCTCTtTACGGAACGAGGGCTGCGGtTGGGCAGGTTGGCTCCTGTCCCCCGCGG

FIGURE 6P

130 US1  
125 T4  
126 US10  
127 T9  
128 T2  
134 S83

125-134 consensus

SEQ ID NO: ISOLATE

131 DK11  
132 SW3  
133 DK8  
129 T8  
130 US1  
125 T4  
126 US10  
127 T9  
128 T2  
134 S83

125-134 consensus

SEQ ID NO: ISOLATE

131 DK11  
132 SW3  
133 DK8  
129 T8  
130 US1  
125 T4  
126 US10  
127 T9  
128 T2  
134 S83

125-134 consensus

SEQ ID NO: ISOLATE

131 DK11  
132 SW3  
133 DK8  
129 T8  
130 US1  
125 T4  
126 US10  
127 T9  
128 T2  
134 S83

125-134 consensus

SEQ ID NO: ISOLATE

131 DK11  
132 SW3  
133 DK8  
129 T8  
130 US1  
125 T4  
126 US10  
127 T9  
128 T2

245 CTTGGCCTCTGTACGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG  
245 CcTGGCCCCCTGTATGGGAATGAGGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG  
245 CtTGGCCCCCTATATGGGAATGAGGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG  
245 CCTGGCCtCTATATGGGAATGAGGGACTCGGCTGGGCgGGATGGCTCCTGTCCCCCGAGG  
245 CTTGGCCCCCTGTATGGGAATGAGGGgCTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG  
245 CtTGGCCCCCTGTATGGGAATGAGGGcCTCGGCTGGGCAGGgTGGCTCCTGTCCCCCGcGG

CtTGGCCcCTgTAtGG-AA-GAGGGc--CGGcTGGGCaGgTGGCTCCTGTCCCCCGcGG

306 GTCTCATCCTAATTGGGGCCCCACTGACCCCCGGCATAaATCACGCAATTTGGGtAAAGTC  
306 GTCTCATCCTAATTGGGGCCCCACTGACCCCCGGCATAGATCACGCAATTTGGGCAAAGTC  
306 GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCATAGATCACGCAATTTGGGCAgAGTC  
306 GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCATAGATCACGTAATTTGGGCAAGGTC  
306 GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCAcAGATCACGTAATTTGGGCAAGGTC  
306 TTCCCGTCCCTCtTGGGGCCCCAaTGACCCCCGGCATAGGTCGCGCAACGTGGGTAAGGTC  
306 TTCCCGTCCCTCTTGGGGCCCCAcTGATCCCCGGCATAGGTCGCGCAACGTGGGTAAGGTC  
306 TTCCCGTCCCTCTTGGGGCCCCAgTGACCCCCGGCATAGGTCGCGCAACGTGGGTAAGGTC  
306 TTCTCGTCCCTCTTGGGGCCCCAaTGACCCCCGGCATAGGTCGCGCAaGTGGGTAAaGTC  
306 TTCTCGcCCTTCaTGGGGCCCCAcGACCCCCGGCATAaATCGCGCAActTGGGTAAGGTC

-TCtCgtCCt-ctTGGGGCCCCActGAcCCCCGGCAtAgaTC-CGcAA-tTGGGtAa-GTC

367 ATCGACACCATTACGTGTGGTTTTGCGGACCTCATGGGGTACATCCCTGTCTGtGGCGCCC  
367 ATCGACACCATTACGTGTGGTTTTGCGGACCTCATGGGGTACATCCCTGTCTGtGGCGCCC  
367 ATCGACACCATTACGTGTGGTTTTGCGGACCTCATGGGGTACATCCCTGTCTGtGGCGCCC  
367 ATCGATACCATTACaTGtGGTTTTGCGGACCTCATGGGGTACATCCCTGTCTGtGGCGCCC  
367 ATCGATACCATTACGTGTGGTTTTGCGGACCTCATGGGGTACATCCCTGTCTGtGGCGCCC  
367 ATCGATACCCTAACGTGCaGcCTTGGCGACCTCATGGGGTACgTCCCCGTCTGtAGCGGcCC  
367 ATCGATACCCTAACGTGCGGCTTTGCGGACCTCATGGGaTACATCCCCGTCTGtGGCGGtC  
367 ATCGATACCCTAACGTGCGGCTTTGCGGACCTCATGGGGTACATCCCCGTCTGtAGGCGCCC  
367 ATCGATACCCTAACGTGCGGCTTTGCGGACCTCATGGGGTACATCCCCGTCTGtAGGCGCCC  
367 ATCGATACCCTAACGTGCGGtTTTGGCGACCTCATGGGGTACATaCCCCGTCTGtGGCGGtC

ATCGAtACC-T-ACgTG-gGtTTTGGCGACCTCATGGGgTACaTcCC-GTCGTtGGCGccC

428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTAGAGTCTCTGGAAGACGGGATAAA  
428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTAGAGTCTCTGGAAGACGGGATAAA  
428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTAGAGTCTCTGGAAGACGGGATAAA  
428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACAcGGTGTAGAGTCTCTGGAAGACGGGATAAA  
428 CGtTgGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGgTCTCTGAGGACGGGGTTAA  
428 CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCAGGCGTGAGAGTCTCTGAGGACGGGGTTAA  
428 CGCTTGGTGGGtGTcGCCAGAGCTCTcGCGCATGGCGTGAGAGTCTCTGAGGACGGGaTTAA  
428 CcgTtGGcGGcGtTcGCCAGAGCcCTcGcCATGGgGTGAGgGTtCTGAGGACGGGaTaAA

CggTtGGaGGcGTcGCCAGAGCTcTgGCaCA-GGtGT-AG-GTcCTGGA-GACGGGaTaAA

489 TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTTCTATCTTCTTACTTGCTCTTCTGTCa  
489 TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTTCTATCTTCTTACTTGCTCTTCTGTcG  
489 TTACGCAACAGGGAATTTGCCTGGTTGCTCTTTTTCTATCTTCTTGGCTTGCTCTTCTGTcG  
489 cTAtGCAACAGGGAATTTGCCTGGTTGCTCTTTTTCTATCTTCTTGGCTTGCTCTTCTGTcCa  
489 TTAcGCAACAGGGAATcTGCTGGTTGCTCTTTTTCTATCTTCTTaCTTGCTCTTCTGTcGg  
489 TTATGCAACAGGGAACtTACCTGGTTGCTCTTTTTCTATcTTCTTGCTGGCCCTACTGTCC  
489 TTATGCAACAGGGAACtTACcGGTTGCTCTTTTTCTATCTTCTTGCTGGCCCTACTGTCC  
489 TTATGCAACAGGGAACcTACcTGGTTGCTCTTTTTCTATCTTCTTGCTGGCCCTACTGTCC  
489 TTATGCAACAGGtAACTTACCCGGTTGCTCctTTTTCTATCTTCTTGCTaGCCCTgCTGTCC



FIGURE 6F

134	S83	489	TTATGCAACgGGgAAAtTTgCCCCGGTTGCTCtTTcTCTATCTTtcTctTgGCCCCtctTGTct
125-134	consensus		tTAtGCAACaGGgAAAtTgCCtGGTTGCTCtTTtTCTATcTTctTgcTtGC-cTtcTGTcc

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
131	DK11	550 TGCTgCACAGTGCCAGTGTCTGCG
132	SW3	550 TGCTtCACAGTGCCAGTGTCTGCG
133	DK8	550 TGCTgCACAGTGCCAGTGTCTGCG
129	T8	550 TGCTtCACAGTGCCAGTGTCTGCA
130	US1	550 TGCgcCACgGTGCCgGTGTCTGCA
125	T4	550 TGCATCACCATTCCAGTCTCcGCT
126	US10	550 TGCATCACCATTCCAGTCTCTGCT
127	T9	550 TGCATCACCacTCCGGcCTCTGCT
128	T2	550 TGCATCACTATTCCGGTTTCaGCT
134	S83	550 TGCATCtCTgTgCCaGTTTCcGCc
125-134	consensus	TGCatCaCagtgCCaGtgTCtGct

0004591.03633  
869350 "T6948050

FIGURE 6G

SEQ ID NO: ISOLATE  
 138 DK12  
 135 HK10  
 136 S52  
 137 S2

135-138 consensus

SEQ ID NO: ISOLATE  
 138 DK12  
 135 HK10  
 136 S52  
 137 S2

135-138 consensus

SEQ ID NO: ISOLATE  
 138 DK12  
 135 HK10  
 136 S52  
 137 S2

135-138 consensus

SEQ ID NO: ISOLATE  
 138 DK12  
 135 HK10  
 136 S52  
 137 S2

135-138 consensus

SEQ ID NO: ISOLATE  
 138 DK12  
 135 HK10  
 136 S52  
 137 S2

135-138 consensus

SEQ ID NO: ISOLATE  
 138 DK12  
 135 HK10  
 136 S52  
 137 S2

135-138 consensus

SEQ ID NO: ISOLATE  
 138 DK12  
 135 HK10  
 136 S52  
 137 S2

135-138 consensus

SEQ ID NO: ISOLATE  
 138 DK12

1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAGAAACACCATCCGTCGCCCACAGG  
 1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAGAAACACCATCCGTCGCCCACAGG  
 1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAGAAACACCATCCGTCGCCCACAGG  
 1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAGAAACACCATCCGTCGCCCACAGG

ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAGAAACACCATCCGTCGCCCACAGG

62 ACGTcAAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG  
 62 ACGTTAAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG  
 62 ACGTTAAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG  
 62 ACaTcAAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG

ACgT-AAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG

123 CCCACGATTGGGTGTGCGCGCGACGCGTAAAACTTCTGAACGGTCaCAGCCTCGCGGACGg  
 123 CCCACGATTGGGTGTGCGCGCGACGCGTAAAACTTCTGAACGGTCgCAGCCTCGCGGACGA  
 123 CCCACGATTGGGTGTGCGCGCGACGCGTAAAACTTCTGAACGGTCACAGCCTCGCGGACGA  
 123 CCCACGATTGGGTGTGCGCGCGACGCGTAAAACTTCTGAACGGTCACAGCCTCGCGGACGg

CCCACGATTGGGTGTGCGCGCGACGCGTAAAACTTCTGAACGGTCaCAGCCTCGCGGACG-

184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGGTCTCTGGGCTCAGCCtGGGTACC  
 184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGGTCTCTGGGCTCAGCCCGGGTACC  
 184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGGTCTCTGGGCTCAGCCCGGGTACC  
 184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGaTCCTGGGCTCAGCCCGGGTACC

CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGgTCCTGGGCTCAGCCcGGGTACC

245 CTTGGCCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGgTGGCTCCTGTCCCCACGCGG  
 245 CTTGGCCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGaTGGCTCCTGTCCCCACGCGG  
 245 CTTGGCCCCCTCTATGGTAAtGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG  
 245 CTTGGCCCCCTCTATGGTAAcGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG

CTTGGCCCCCTCTATGGTAAcGAGGGCTGCGGGTGGGCAGGgTGGCTCCTGTCCCCACGCGG

306 CTCCCGTCCATCTTGGGGCCCAACGACCCCCGGCGgaGGTCCCGCAATTTGGGTAAgGTC  
 306 CTCCCGTCCATCTTGGGGCCCAACGACCCCCGGCGGaCGGTCCCGCAATTTGGGTAAAGTC  
 306 CTCCCGTCCATCTTGGGGCCCAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  
 306 CTCCCGTCCATCTTGGGGCCCAAtGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC

CTCCCGTCCATCTTGGGGCCCAAcGACCCCCGGCGgaGGTCCCGCAATTTGGGTAAgGTC

367 ATCGATACCCTcACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC  
 367 ATCGATACCCTTACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC  
 367 ATCGATACCCTTACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC  
 367 ATCGATACCCTTACGTGCGGcTTGCGCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC

ATCGATACCCTcACGTGCGGaTTGCGCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC

428 CtGTAGGgGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA

FIGURE 6G

135 HK10  
136 S52  
137 S2

135-138 consensus

SEQ ID NO: ISOLATE

138 DK12  
135 HK10  
136 S52  
137 S2

135-138 consensus

SEQ ID NO: ISOLATE

138 DK12  
135 HK10  
136 S52  
137 S2

135-138 consensus

428 CCGTAGGAGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA  
428 CCGTAGGAGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA  
428 CCGTAGGAGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA

CcGTAGGaGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA

489 TTTCGCAACAGGGAACCTTGCCCGGTTGCTCCTTTTCTATCTTCCTTCTTGCTCTGTTCTCT  
489 TTTCGCAACAGGGAACCTTGCCCGGTTGCTCCTTTTCTATCTTCCTTCTTGCTCTGTTCTCT  
489 TTTTGCAACAGGGAACCTTGCCCGGTTGCTCCTTTTCTATCTTCCTTCTTGCTCTGTTCTC  
489 TTTTGCAACAGGGAACCTTGCCCGGTTGCTCtTTTTCTATCTTCCTTCTTGCCtGTTCTCt

TTT-GCAACAGGGAACCTTGCCCGGTTGCTCtTTTTCTATCTTCCTTCTTGCTcTGTTCTCt

550 TGCcTAATTCATCCAGCAGCTAGT  
550 TGCTTAATTCATCCAGCAGCTAGT  
550 TGCTTAgtTTCATCCtGCAGCTAGT  
550 TGCTTAaTTCATCCaGCAGCTAGT

TGCTTAaTTCATCCaGCAGCTAGT

09084591.052698

FIGURE 6H

SEQ ID NO: ISOLATE

145 DK13  
143 Z6  
144 Z7  
140 Z8  
139 Z4  
142 Z5  
141 Z1

139-145 consensus

1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCaATGG  
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCATGG  
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCATGG  
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCATGG  
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCATGG  
1 ATGAGCACaATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGcCGCCCATGG

ATGAGCACgAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGcCGCCCaATGG

SEQ ID NO: ISOLATE

145 DK13  
143 Z6  
144 Z7  
140 Z8  
139 Z4  
142 Z5  
141 Z1

139-145 consensus

62 ACGTTAAGTTCCCGGGTGGcGGCCAGATCGTTGGCGGAGTTTACTTGTGTCGCGCAGGGG  
62 ACGTTAAGTTCCCGGGTGGTGGCCAGATCGTTGGCGGAGTTTACTTGTGTCGCGCAGGGG  
62 ACGTTAAGTTCCCGGGCGGTGGCCAGATCGTTGGCGGAGTTTACTTGTGTCGCGCAGGGG  
62 AtGTAAaATCCCaGGCGGcGGCCAGATCGTTGGCGGAGTTTACTTGTGTCGCGCAGGGG  
62 AcGTAAaATCCCGGGTGGTGGCCAGATCGTTGGCGGAGTTTACTTGTGTCGCGCAGGGG  
62 ATGTAAaATCCCGGGTGGTGGtCAGATCGTTGGCGGAGTTTACTTGTGTCGCGCAGGGG  
62 ATGTgAAATCCCGGGcGGcGGcCAGATCGTTGGCGGAGTTTACTTGTcTGCCGCGCAGGGG

AcGT-AAgTTCCCGgGGtGGtGGcCAGATCGTTGGCGGAGTTTACTTGTcTGCCGCGCAGGGG

SEQ ID NO: ISOLATE

145 DK13  
143 Z6  
144 Z7  
140 Z8  
139 Z4  
142 Z5  
141 Z1

139-145 consensus

123 CCCTAGaTTGGGTGTGCGCGGACTAGGAAGACTTCGGAGCGGTTCGCAACCTCGTGGGAGg  
123 CCCcAGgTTGGGTGTGCGCGGACTAGGAAGACTTCGGAGCGGTTCGCAACCTCGTGGGAGA  
123 CCCcAGaTTGGGTGTGCGCaCaACTAGGAAGACTTCGGAGCGGTTCGCAACCTCGTGGGAGA  
123 CCCcAGgTTGGGTGTGCGCGGACTCGGAAGACTTCGGAGCGGTTCGCAACCTCGTGGCAGG  
123 CCCcAGgTTGGGTGTGCGCGGACTCGaAAGACTTCGGAGCGGTTCGCAACCTCGTGGCAGG  
123 CCCcAGgTTGGGTGTGCGCGGACTCGGAAGACTTCGGAGCGGTTCGCAACCTCGcGGCAGG  
123 CCCcGGTTGGGTGTGCGCGCagCTCGGAAGACTTCGGAGCGGTTCaCAACCTCGtGGCAGG

CCCcAGgTTGGGTGTGCGCGcGgaCTcGgAAGACTTCGGAGCGGTTCgCAACCTCGtGGcAGg

SEQ ID NO: ISOLATE

145 DK13  
143 Z6  
144 Z7  
140 Z8  
139 Z4  
142 Z5  
141 Z1

139-145 consensus

184 CGCCAGCCTATCCCCAAGGCgCGcCaActcGAGGGtAGGTCTCTGGGCTCAGCCtGGGTATC  
184 CGCCAGCCTATCCCCAAGGCACGTCTGAGGGAAGGTCTCTGGGCTCAGCCCGGGTATC  
184 CGTCAGCCTATCCCCAAGGCACGTCTGAGGGAAGGTCTCTGGGCTCaACCCGGGTACC  
184 CGTCAGCCTATCCCCAAGGCACGTCTGGTCcGAGGGtAGGTCTCTGGGCTCAGCCCGGGTACC  
184 CGTCaACCTATCCCCAAGGCgCGcCaGcCaGAGGGCAGaTCCTGGGCGcCAGCCCGGGTACC  
184 CGTCAGCCTATCCCCcAGGCaCGtCGGTCCGAGGGCAGGTCTCTGGGCTCAGCCCGGGTACC  
184 CGTCAGCCTATCCCCaAGGCgCGcCGGTCCGAGGGCAGGTCTCTGGGCTCAGCCCGGGTACC

CGtCAgCCTATCCCCaAGGCaCGtCggtccGAGGGcAGgTCCTGGGCTCaGCCCcGGGTACc

SEQ ID NO: ISOLATE

145 DK13  
143 Z6  
144 Z7  
140 Z8  
139 Z4  
142 Z5  
141 Z1

139-145 consensus

245 CtTGGCCcCTTTACGGcAATGAGGGcTGCGGGTGGGCGGGATGGCTCCTGTcACCCCGTGG  
245 CATGGCCTCTTTACGGTAATGAGGGTTCGCGGTGGGCGGGATGGCTCCTGTcACCCCGTGG  
245 CATGGCCTCTTTACGGTAATGAGGGTTCGCGGTGGGCGGGATGGCTCtTGTCACCCCGTGG  
245 CATGGCCTCTTTACGGTAATGAaGGCTGtGGGTGGGCAGGtTGGCTCCTGTcCCCCGCGG  
245 CTTGGCCcCTcTATGGCAATGAGGGCTGcGGGTGGGCAGGGTGGCTCCTGTcCTcCGCGG  
245 CTTGGCCTCTTTATGGCAATGAGGGCTGTGGGTGGGCAGGGTGGCTCCTGTCCCCCGCGG  
245 CTTGGCCcCTTTAcGGCAATGAGGGCTGTGGGTGGGCAGGGTGGCTCCTGTCCCCCGCGG

CtTGGCCTCTtTAcGGcAATGAGGGcTGcGGGTGGGCAGG-TGGCTCtTGTC-CCcCGcGG

SEQ ID NO: ISOLATE

145 DK13  
143 Z6  
144 Z7  
140 Z8

306 CTCTCGgCCGTCTTGGGGcCCgAATGATCCCCGGCGgAGGTCCCGCAACTTGGGTAAGGTC  
306 CTCTCGACCGTCTTGGGGcCCAAATGATCCCCGGCGAAGGTCCCGCAACTTGGGTAAGGTC  
306 CTCTCGACCGTCTTGGGGcCCAAATGATCCCCGGCGAAGGTCCCGCAACTTGGGTAAGGTC  
306 CTCTCGACCGTCTTGGGGcCCAAATGATCCCCGGCGAAGGTCCCGCAATTGGGTAAGGTC

FIGURE 6H

139 Z4  
142 Z5  
141 Z1

139-145 consensus

306 CTCTCGGCCATCTTGGGGCCCAATGATCCCCGGCGGAGaTCGCGCAATCTGGGTAAGGTC  
306 aTCTCGGCCATCTTGGGGCCaAAATGATCCCCGGCGTAGGTCCCGCAATCTGGGTAAGGTC  
306 tTCcaGGCCgTCTTGGGGCCcAAATGATCCCCGGCGTAGGTCCCGtAATCTGGGTAAaGTC

cTctcGgCCgTCTTGGGGcCcaAAATGATCCCCGGCGgAGgTCcCGcAAAtTGGGTAAGGTC

SEQ ID NO: ISOLATE

145 DK13  
143 Z6  
144 Z7  
140 Z8  
139 Z4  
142 Z5  
141 Z1

139-145 consensus

367 ATCGATACcCTAACTTGGCGcTTCGCCGAcCTCATGGGATACATCCCGgTCGTAGGCGCCCC  
367 ATCGATACtCTAACTTGGCGtTTCGCCGAtCTCATGGGATACATCCCGCTCGTAGGCGCCCC  
367 ATCGATACCCTAACcTGCGGCTTtGCCGACCTCATGGGATACATCCCGCTCGTAGGCGCCCC  
367 ATCGATACCCTcACGTGCGGCTTCGCCGACCTCATGGGATACATCCCGCTCGTGGGCGCCCC  
367 ATCGATACCCTGACGTGCGGCTTCGCCGACCTCATGGGATACATCCCGaTCGTGGGCGCCCC  
367 ATCGATACCCTGACGTGTGGCTTCGCCGACCTCATGGGATACATTCCGCTCGTcGGGCGCCCC  
367 ATCGATACCCTGACGTGTGGCTTCGCCGACCTCATGGGATACATTCCGCTCGTaGGGCGCCCC

ATCGATACcCT-ACgTGcGGcTTCGCCGAcCTCATGGGATACATcCCGcTCGTaGGGCGCCCC

SEQ ID NO: ISOLATE

145 DK13  
143 Z6  
144 Z7  
140 Z8  
139 Z4  
142 Z5  
141 Z1

139-145 consensus

428 CCGTGGGtGGCGTCGCCAGaGCCCTGGCGCATGGcGTcAGGcTcTcTGGAGGACGGGgTCAA  
428 CCGTGGGCGGCGTCGCCAGGGCCCTGGCaCATGGtGTTAGGGCTgTGGAGGACGGGATCAA  
428 CCGTGGGCGGCGTCGCCAGGGCCCTaGCGCATGGCGTTAGGGCTcTGGAGGACGGGATtAA  
428 CaGTaGgaGGCGTCGCCAGaGCCCTGGCGCATGGCGTCAGGGCTGTGGAGGACGGGATcAA  
428 CcGTgGGgGGCGTCGCCAGGGCctCTGGCGCATGGCGTCAGGGCTGTGGAGGACGGGATtAA  
428 CaGTaGGTGGCGTCGCCAGGGCCtTGGCGCATGGCGTCAGGGCCcTGGAGGACGGAATcAA  
428 CtGTgGGTGGCGTCGCCAGGGCCcTGGCGCATGGCGTCAGGGCCgTGGAGGACGGAATtAA

CcGTgGGtGGCGTCGCCAGgGCcTgGCgCATGGcGTcAGGgctgTGGAGGACGGgaTcAA

SEQ ID NO: ISOLATE

145 DK13  
143 Z6  
144 Z7  
140 Z8  
139 Z4  
142 Z5  
141 Z1

139-145 consensus

489 TTATGCAACAGGGAATCTTCCCGTTGCTCTTTCTCTATCTTCCTCTTGGCACTgCTcTCG  
489 TTATGCAACAGGGAATCTTCCCGTTGCTCTTTCTCTATCTTCCTCTTGGCACTTCTTTTCG  
489 TTATGCAACAGGGAACCTTCCCGTTGCTCTTTtTCTATCTTCCTCTTGGCACTTCTTTTCG  
489 CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTCTTGGCACTTCTcTCG  
489 CTATGCAACAGGGAATCTTCCcGGTTGCTCTTTCTCTATCTTCCTtTGGCACTTCTcTCG  
489 CTATGCAACAGGGAATCTTCTGGTTGCTCctTtTCTATCTTCCTaCTTGCACTTtTCTCG  
489 CTAcGCAACAGGGAACCTTCCCTGGTTGCTCctTtTCTATCTTtCTtCTTGCACTTtTCTCG

cTAtGCAACAGGGAAtCTTCCcGGTTGCTCctTtTCTATCTTcCTctTgGCACTtctcTCG

SEQ ID NO: ISOLATE

145 DK13  
143 Z6  
144 Z7  
140 Z8  
139 Z4  
142 Z5  
141 Z1

139-145 consensus

550 TGCCTgACTGTTCCCGcTTCGGCC  
550 TGCCTaACTGTTCCCaCCTCGGCC  
550 TGCCTgACTGTTCCCGCCTCGGCC  
550 TGCCTaACcGTcCCAGCGTcTcGCT  
550 TGCCTcACtGTtCCAGCGTCgGCT  
550 TGCTTGACAACACCgGCATCcgGCT  
550 TGCcTGACAACACCgGCATCtGCC

TGCcTgACTgttCC-gC-TCgGCC

FIGURE 6I

SEQ ID NO: ISOLATE

153 SA11  
152 SA6  
146 SA4  
147 SA5  
148 SA7  
149 SA1  
150 SA3  
151 SA13

146-153 consensus

1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCaaAAGAAACACCAACCGCCGCCACAGG  
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCaaAAGAAACACCAACCGCCGCCACAGG  
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACCAACCGCCGCCACAGG  
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACCAACCGCCGCCACAGG  
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACCAACCGCCGCCACAGG  
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACCAACCGCCGCCACAGG  
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACCAACCGCCGCCACAGG  
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACCAACCGCCGCCACAGG

ATGAGCACGAATCCTAAACCTCAAAGAAAAACCaaAAGAAACACCAACCGCCGCCACAGG

SEQ ID NO: ISOLATE

153 SA11  
152 SA6  
146 SA4  
147 SA5  
148 SA7  
149 SA1  
150 SA3  
151 SA13

146-153 consensus

62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTGTGCCGCGCAGGGG  
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTGTGCCGCGCAGGGG  
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTGTGCCGCGCAGGGG  
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTGTGCCGCGCAGGGG  
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTGTGCCGCGCAGGGG  
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTGTGCCGCGCAGGGG  
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTGTGCCGCGCAGGGG  
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTGTGCCGCGCAGGGG

ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTGTGCCGCGCAGGGG

SEQ ID NO: ISOLATE

153 SA11  
152 SA6  
146 SA4  
147 SA5  
148 SA7  
149 SA1  
150 SA3  
151 SA13

146-153 consensus

123 CCCTaGgtTGGGTGTGCGCGGACTCGGAAGACTTCaGAACGGTCGCAACCCCGTGGgCGG  
123 CCCTeGtaTGGGTGTGCGCGGACTCGGAAGACTTCgGAACGGTCGCAACCCCGTGGgCGG  
123 CCCTAGgtTGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG  
123 CCCTAGaTTGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG  
123 CCCTAGgTTGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG  
123 CCCAGGTTGGGTGTGCGCGGACTCGGAAGACTTCgGAACGGTCGCAACCCCGTGGGCGG  
123 CCCAGGTTGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG  
123 CCCtAGGTTGGGTGTGCGCGCaACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGACGG

CCCTaGgtTGGGTGTGCGCGGACTCGGAAGACTTCaGAACGGTCGCAACCCCGTGGgCGG

SEQ ID NO: ISOLATE

153 SA11  
152 SA6  
146 SA4  
147 SA5  
148 SA7  
149 SA1  
150 SA3  
151 SA13

146-153 consensus

184 CGTCAGCCTATTCCCAAGGCGCGCAaCCaCGGGcCGGTCTGGGGTCAACCCGGGTACC  
184 CGTCAGCCTATTCCCAAGGCGCGCAaTCCgCGGGtCGGTCTGGGGTCAACCCGGGTACC  
184 CGCCAGCCTATTCCCAAGGCGCGCAACCCACGGGCCGGTCTGGGGTCAACCCGGGTACC  
184 CGCCAGCCTATTCCCAAGGCGCGCAACCCACGGGCCGGTCTGGGGTCAACCCGGGTACC  
184 CGCCAGCCTATTCCCAAGGCGCGCAACCCACGGGCCGGTCTGGGGTCAACCCGGGTACC  
184 CGCCAGCCTATTCCCAAGGcCGCCAGCCCACGGGCCGGTCTGGGGTCAACCCGGGTACC  
184 CGtCAGCCTATtCCCAAGGcCGCCAGCCCACGGGCCGGTCTGGGGTCAACCCGGGTACC

CGcCAGCCTATtCCCAAGGcCGCCaCCaCGGGcCGGTCTGGGGTCAACCCGGGTACC

SEQ ID NO: ISOLATE

153 SA11  
152 SA6  
146 SA4  
147 SA5  
148 SA7  
149 SA1  
150 SA3  
151 SA13

146-153 consensus

245 CTTGGCCCCtTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGtTGCTCTCCCCtCGAGG  
245 CTTGGCCCCTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGTTGCTCTCCCCCGAGG  
245 CTTGGCCCCTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGTTGCTCTCCCCCGAGG  
245 CTTGGCCCCTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGTTGCTCTCCCCCGAGG  
245 CTTGGCCCCTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGTTGCTCTCCCCCGAGG  
245 CTTGGCCCCTTTACGCCAATGAGGGCCTCGaGTGGGCAGGGTGGTTGCTCTCCCCCGAGG  
245 CTTGGCCCCTTTACGCCAATGAGGGCCTCGgGTGGGCAGGGTGGTTGCTCTCCCCCGAGG  
245 CTTGGCCCCTTTAtGCCAATGAGGGCCTCGgGTGGGCAGGGTGGTTGCTCTCCCCCGAGG

CTTGGCCCCtTTTAcGCCAATGAGGGCCTCGgGTGGGCAGGGTGGtTGCTCTCCCCcCGAGG

FIGURE 6I

SEQ ID NO: ISOLATE

153 SA11  
152 SA6  
146 SA4  
147 SA5  
148 SA7  
149 SA1  
150 SA3  
151 SA13

146-153 consensus

SEQ ID NO: ISOLATE

153 SA11  
152 SA6  
146 SA4  
147 SA5  
148 SA7  
149 SA1  
150 SA3  
151 SA13

146-153 consensus

SEQ ID NO: ISOLATE

153 SA11  
152 SA6  
146 SA4  
147 SA5  
148 SA7  
149 SA1  
150 SA3  
151 SA13

146-153 consensus

SEQ ID NO: ISOLATE

153 SA11  
152 SA6  
146 SA4  
147 SA5  
148 SA7  
149 SA1  
150 SA3  
151 SA13

146-153 consensus

SEQ ID NO: ISOLATE

153 SA11  
152 SA6  
146 SA4  
147 SA5  
148 SA7  
149 SA1  
150 SA3  
151 SA13

146-153 consensus

306 CTCTCGGCCTAAcTGGGGCCCCAATGACCCCCGGCGAAgATCGCGCAATTTGGGcAAGGTC  
306 CTCTCGGCCTAATTGGGGCCCCAATGACCCCCGGCGAAAATCGCGCAATTTGGGTAAGGTC  
306 CTCTCGGCCTAATTGGGGCCCCAATGACCCCCGGCGAAAATCGCGCAATTTGGGTAAGGTC  
306 CTCTCGGCCTAATTGGGGCCCCAATGACCCCCGGCGAAAATCGCGCAATTTGGGTAAGGTC  
306 CTCTCGGCCTAATTGGGGCCCCAATGACCCCCGGCGAAAATCGCGCAATTTGGGTAAGGTC  
306 CTCTCGGCCTAATTGGGGCCCCAATGACCCCCGGCGAAAATCGCGCAATTTGGGTAAGGTC  
306 CTCTCGGCCTAATTGGGGCCCCAATGACCCCCGGCGAAAATCGCGCAATTTGGGTAAGGTC  
306 CTCTCGGCCTAATTGGGGCCCCAATGACCCCCGGCGAAAATCGCGCAATTTGGGTAAGGTC

CTCTCGGCCTAatTGGGGCCCCAatGACCCCCGGCGaAaaTCGCGCAatTTGGGtAAGGTC

367 ATCGATACCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC  
367 ATCGATACCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC  
367 ATCGATACCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC  
367 ATCGATACCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC  
367 ATCGATACCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC  
367 ATCGATACCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC  
367 ATCGATACCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC  
367 ATCGATACCCTgACGTGCGGATTGCGCGAcCTCATGGGGTACATCCCGCTCGTAGGCGGCC

ATCGAtACCCTaACgTGCGGATTGCGCGAcCTCATGGGGTACATCCCGCTCGTAGGCGGCC

428 CCGTTGGGGGCGTCGCAAGGGCcCTCGCACACGGTGTGAGaGcCTTGAGGACGGGGTAAA  
428 CCGTTGGGGGCGTCGCAAGGGCcCTCGCACACGGTGTGAGGGTTCTTGAGGACGGGGTAAA  
428 CCGTTGGGGGCGTCGCAAGGGCCCTtGCACATGGTGTGAGGGTTCTTGAGGACGGGGTAAA  
428 CCGTTGGGGGCGTCGCAAGGGCCCTCGCACATGGTGTGAGGGTTCTTGAGGACGGGGTAAA  
428 CCGTTGGGGGCGTCGCAAGGGCTCTCGCACACGGTGTGAGGGTTCTTGAGGACGGGGTAAA  
428 CCGTTGGGGGCGTCGCAAGGGCTCTCGCACAcGGTGTGAGGGTTCTTGAGGACGGGGTAAA  
428 CCGTTGGGGGCGTCGCAAGGGCTCTCGCACAcGGTGTGAGGGTcCTTGAGGACGGGGTAAA

CCGTTGGGGGCGTCGCAAGGGCcCTcGCACAcGGTGTGAGgGtCTTGAGGACGGGGTAAA

489 tTATGCAACAGGGAATcTtCCCCGGTTGCTCTTTCTCtATCTTTaTCCTTGCACTTCTCTCG  
489 CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTTgTCCTTGCACTTCTCTCG  
489 CTATGCAACgGGAATTTGCCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTCTCG  
489 CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTCTCG  
489 tTACGCAACAGGGAATcTGCCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTCTCG  
489 CTACGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTTTTc  
489 CTACGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTTTCA  
489 CTAtGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTTTCA

cTAtGCAACaGGAATtTgCCCCGGTTGCTCTTTCTCtATCTTTaTCCTTGCACTTCTcTCg

550 TGcTgACCGTCCCgGCCaCTGCA  
550 TGCCTaACCGTCCCtGCCTCTGCA  
550 TGCCTGACCGTCCCgGCCTCTGCA  
550 TGcTgACCGTCCCAGCCTCTGCA  
550 TGCCTGACCGTCCCAGCCTcGCA  
550 TGtCTGAtCaTCCCGGCCTCTGCA  
550 TGCCTGACCGTCCCgGCCTCTGCA  
550 TGCCTGACTGTCCCGaCCTCTGcC

TGccTgAccgTCCCgGCtCtGCa

FIGURE 6J

SEQ ID NO: Genotype  
103-154 cons.

103-124 1  
125-134 2  
135-138 3  
139-145 4  
146-153 5  
154 6

1 ATGAGCACgaaTCCTAAACCTCAAAGAAaAaACCaaAcGtAAcACcAaCCgcCGCCcAcagG  
1 ATGAGCACgAaTCCTAAACCTCAAAGAAaAaACCaaACGTAACACCAaCCgcCGCCcACAGG  
1 ATGAGCACAAaTCCTAAACCTCAAAGAAAAACCAaAGAAAcACaAACCGcCGCCcACagG  
1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAAGAAACACCATCCGTCGCCcACAGG  
1 ATGAGCACgAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGcCGCCcATGG  
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAaAGAAACACCAACCGcCGCCcACAGG  
1 ATGAGCACACTTCCAAACCCCAAAGAAAAACCAAAAGAAACACCAACCGTCGCCcAACGG

SEQ ID NO: Genotype  
103-154 cons.

103-124 1  
125-134 2  
135-138 3  
139-145 4  
146-153 5  
154 6

62 AcgTcAAgTTcCCgGGcGGtGGtCAGATCGTtGGtGGAGTtTAcTtGtTGCCGCGCAGGGG  
62 ACGTcAAGTTCCCGGGcGGtGGtCAGATCGTtGGTGGAGTtTAcTtGtTGCCGCGCAGGGG  
62 ACGTtAAGTTcCCGGGcGGcGGcCAGATCGTtGGCGGAGTtTAcTtGtTGCCGCGCAGGGG  
62 ACGTcAAGTTCCCGGGTGGCGGACAGATCGTtGGTGGAGTtTAcTtGtTGCCGCGCAGGGG  
62 AcGTaAAgTTCCCGGGtGGtGGcCAGATCGTtGGCGGAGTtTAcTtGtTGCCGCGCAGGGG  
62 ACGTcAAGTTCCCGGGcGGTGGTcAGATCGTtGGTGGAGTtTAcTtGtTGCCGCGCAGGGG  
62 ACGTCAAGTTCCCGGGTGGCGGTcAGATCGTtGGCGGAGTtTAcTtGtTGCCGCGCAGGGG

SEQ ID NO: Genotype  
103-154 cons.

103-124 1  
125-134 2  
135-138 3  
139-145 4  
146-153 5  
154 6

123 CCCcaGgtTGGGTGTGCGCGcGgaCtaGgAAgaCTTCcGAgCGgTCgCAaCCtcGtGGaaGg  
123 CCCcaGgtTGGGTGTGCGCGcGgaCtaGgAAgACTTCcGAGCGgTCgCAaCCTCGtGGaaGg  
123 CCCcAGgTTGGGTGTGCGCGcGgACaAGGAgaCTTCcGAgCGaTCCAGCCgCGTGGgAGg  
123 CCCACGATTGGGTGTGCGCGcGACCGCTAAaACTTCGAACGGTcCaCAGCCTCGCGGACGa  
123 CCCcaGgtTGGGTGTGCGCGcGgaCTcGgAAGACTTCGAGCGGTcCaCAGCCTCGtGGcAGg  
123 CCCtaGgtTGGGTGTGCGCGcGgACTCGGAAGACTTCaGAACGGTCGCAACCCCGTGGgCGG  
123 CCCCCGgtTGGGTGTGCGCGcGACGAGAAAGACTTCGAGCGATCCAGCCcAGAGGCAGG

SEQ ID NO: Genotype  
103-154 cons.

103-124 1  
125-134 2  
135-138 3  
139-145 4  
146-153 5  
154 6

184 CGaCAGCCTATcCCcaAgGctCGcCggccccgagGGcaggtcCTGGGctcagCCcGGgtAcC  
184 CGaCAaCCTATCCCCAAGGctCGcCggCCCCGAGGGcAGGgCCTGGGctCAGCCcGGGtAcC  
184 CGCCAGCCCCATCCCgAAAGATCGGCGctCCAcTGGCAAGtCCTGGGGAAaCCaGGATATc  
184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGGAAGGCCGgTCCTGGGCTCAGCCcGGGTACC  
184 CGtCAGCCTATCCCCaAGGcAGtCggtccGAGGGcAGgTCCTGGGCTCAGCCcGGGTACC  
184 CGcCAGCCTATcCCCAAGGcCGCCaAcCCaCGGcCGGTCTGGGGTCAACCCGGGTACC  
184 CGCCAACCTATACCAAGGCGCGCCAGCCCCAGGGCAGGCACTGGGCTCAGCCCGGATACC

SEQ ID NO: Genotype  
103-154 cons.

103-124 1  
125-134 2  
135-138 3  
139-145 4  
146-153 5  
154 6

245 CtTGGCCcCtTAtGgcaAtGAGGGcttcGggTGGGCaGGaTGGcTccTgTCCcCgcGG  
245 CtTGGCCCCCTAtGgCaAtGAGGGcttcGggTGGGCaGGATGGCTCCTGTcACCCcgtGG  
245 CtTGGCCcCTgTAtGGgAAtGAGGGcctCGGcTGGGCaGGtTGGCTCCTGTCCCCCGcGG  
245 CTTGGCCCCCTATGGTAACGAGGGCTGCGGGTGGGcAGGgTGGCTCCTGTCCCCACGCGG  
245 CtTGGCCcCTtTAcGGcAAtGAGGGcTgCGGGTGGGCaGGgTGGCTCCTGTCCcCGcGG  
245 CTTGGCCCCcTTTAcGCCAATGAGGGCTCGgTGGGcAGGGTGGtTGCTCTCCCCcCGAGG  
245 CTTGGCCTCTTTATGGAAACGAGGGCTGTGGGTGGGcAGGtTGGCTCCTGTCCCCCGCGG

SEQ ID NO: Genotype  
103-153 cons.

103-124 1  
125-134 2  
135-138 3  
139-145 4  
146-153 5  
154 6

306 cTCtcggCCtagtTGGGGcCccActGAcCCCCGGCgtaggTCgCGcAAAttTGGGtAagGTC  
306 cTCtcCGGCCTAgTGGGGCCCCcAcaGACCCCCGGCGtAGGTTCGCGtAAAttTGGGtAAGGTC  
306 tTCtCgtCCtctTGGGGCCCCActGAcCCCCGGCAtAgATCgCGcAAAttTGGGtAagGTC  
306 CTCCCGTCCATCTTGGGGCCCCAAAcGACCCCCGGCGgaAGGTCCCGCAATTGGGTAAAGTC  
306 cTCtcGgCCgTCTTGGGGcCcaAATGATCCCCGGCGgAGgTCcCGcAAAttTGGGTAAAGTC  
306 CTCTCGGCCTAAtTGGGGCCCCAAtGACCCCCGGCGaAaaTCGCGCAAtTGGGTAAAGGTC  
306 CTCCCGGCCACATTGGGGCCCCAATGACCCCCGGCGTCGATCCCGGAATTGGGTAAAGGTC



FIGURE 6J

SEQ ID NO: Genotype  
103-154 cons.

103-124 1  
125-134 2  
135-138 3  
139-145 4  
146-153 5  
154 6

367 ATCGAtACcctACgTGcgGctTcGCCGAcCTCATGGGgTACaTcCCGcTCGTcGGcGccc  
367 ATCGAtACCCTcACaTGCGGCTTcGCCGACCTCATGGGGTACATtCCGCTCGTCGGcGccc  
367 ATCGAtACCcTaACgTGcgGttTTGCCGACCTCATGGGgTACaTcCCcGTCGTtGGCGccc  
367 ATCGATACCCTtACGTGCGGaTTCCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC  
367 ATCGATACcCTgACgTGcGGcTTcGCCGAcCTCATGGGATACATcCCGcTCGTaGGCGCCC  
367 ATCGAtACCCTaACgTGCGGATTCCGCCGAcCTCATGGGGTACATCCCGCTCGTAGGCGGCC  
367 ATCGATACCCTAACGTGTGGGTTCCGCCGATCTCATGGGGTACATtCCCGTCGTGGGCGCGC

SEQ ID NO: Genotype  
103-154 cons.

103-124 1  
125-134 2  
135-138 3  
139-145 4  
146-153 5  
154 6

428 CcgTaGGgGGcGtcGCCaggGCCcTgGCgCatGGcGTcaGggttcTgGAgGACGGgTgAA  
428 CccTaGGgGGcGcTGCCAGgGCCcTGGCgCatGGcGTCCGgGTtCTGGAgGACGGCGTGAA  
428 CggTtGGaGGcGTcGCCAGAGCtCTgGCaCatGGtGTgAGgGTcCTGGAGGACGGGaTaaa  
428 CcGTAGGaGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA  
428 CcGTgGGtGGCGTCGCCAGgGCCcTgGCgCATGGcGTcAGGgctgTGGAGGACGGGaTcAA  
428 CCGTTGGGGGCGTCGCAAGGGCtCTcGCACAcGGTGTGAGgGttCTTGAGGACGGGGTAAA  
428 CTTTGGGCGGCGTCGCGCTCGCCTCGCACATGGCGTGAGGGCAATCGAGGACGGGATCAA

SEQ ID NO: Genotype  
103-154 cons.

103-124 1  
125-134 2  
135-138 3  
139-145 4  
146-153 5  
154 6

489 cTatGCAACaGGgAAAttTgCCcGGTTGCTCtTTcTCTATcTTccTccTgGCTcTgcTgTCC  
489 cTAtGCAACAGGGAAtcTgCCcGGTTGCTCtTTcTCTATCTTCCtctTgGCTtTgcTgTCC  
489 tTAtGCAACaGGgAAAttTgCCcGGTTGCTCtTTtTCTATcTTctTgcTtGCccTtcTGTCc  
489 TTTcGCAACAGGGAActTGCCCGGTTGCTCtTTTTCTATCTTCCtTCTTGCTCTGTTCCTc  
489 cTAtGCAACAGGGAAtCTTCCcGGTTGCTCtTTcTCTATCTTcCTctTgGCACTtctTcTCG  
489 cTAtGCAACaGGGAAtTgCCCGGTTGCTCTTTCTCTATCTTTaTCCTTGCACTTCTcTCg  
489 TTATGCAACAGGGAATCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTGGCACTACTCTCG

SEQ ID NO: Genotype  
103-154 cons.

103-124 1  
125-134 2  
135-138 3  
139-145 4  
146-153 5  
154 6

550 TGcctgaccgctcCCagcttCtgct  
550 TGttTgACcatcCCaGctTCcGCT  
550 TGCatCaCagtGCCaGtgTCTGCT  
550 TGCTTAaTTCATCCaGCAGCTAGT  
550 TGCcTgACtggtCCagCgTCgGCC  
550 TGccTgAccgTCCCgGCCtCtGCa  
550 TGCCTCACAACGCCAGCTTCGGCT

09084691.052598

[illegible]

HSEQ ID NO:	Genotype
103-108	I/1a
109-124	II/1b
125-128	III/2a
129-133	IV/2b
134	2c
135-138	3a
139	4a
141	4b
143	4c
145	4d
142	4e
146	4f
147-150	5a
146-153	5a
154	6a

FIGURE 6A

SEQ ID NO:	Genotype	350	360	370	380	390	400	410	420	430	440	450	460
103-108	I/1a	TCGCGCAATTGGGTAAAGTTCATCGATAGCCTCAGTGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTGGCGCCGCCCGTGGCGGGCCCTGGCGCATG											
109-124	I/1b												
125-128	I/1/2a												
129-133	I/2b												
134	2c												
135-138	(V)/3a												
139	4a												
141	4b												
143	4c												
145	4d												
142	4e												
140	4f												
146-153	5a												
154	6a												

SEQ ID NO:	Genotype	470	480	490	500	510	520	530	540	550	560	570
103-108	I/1a	GcGTcaggggttcTgAGGACGCGggTgAAcTatGCAACaGggaattTgCCCGTGGCTTCTCTATCTTccTccTgGCTcTgTgTcTlGcctgacggtccGagctttGct										
109-124	I/1b											
125-128	I/1/2a											
129-133	I/2b											
134	2c											
135-138	(V)/3a											
139	4a											
141	4b											
143	4c											
145	4d											
142	4e											
140	4f											
146-153	5a											
154	6a											

FIGURE 7A

SEO ID NO: ISOLATE  
 156 US11  
 157 S14  
 158 SW1  
 159 S18  
 160 DR4  
 155 DK7

155-160 consensus

1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR  
 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR  
 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR  
 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR  
 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR  
 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR

SEO ID NO: ISOLATE  
 156 US11  
 157 S14  
 158 SW1  
 159 S18  
 160 DR4  
 155 DK7

155-160 consensus

62 RQIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV  
 62 RQIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV  
 62 RQIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV  
 62 RQIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV  
 62 RQIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV  
 62 RQIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV

RQIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV

SEO ID NO: ISOLATE  
 156 US11  
 157 S14  
 158 SW1  
 159 S18  
 160 DR4  
 155 DK7

155-160 consensus

123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS  
 123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS  
 123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS  
 123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS  
 123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS  
 123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS

IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS

SEO ID NO: ISOLATE  
 156 US11  
 157 S14  
 158 SW1  
 159 S18  
 160 DR4  
 155 DK7

155-160 consensus

184 CLTVPASA  
 184 CLTVPASA  
 184 CLTVPASA  
 184 CLTVPASA  
 184 CLTVPASA  
 184 CLTVPASA

CLTVPASA

0908493.052593

[illegible]

<u>SEQ</u>	<u>ID NO:</u>	<u>ISOLATE</u>
175		P8
170		IND8
162		S45
171		S9
163		D1
165		P10
169		IND3
164		US6
166		DK1
167		T10
168		SW2
161		SA10
174		HK4
172		HK3
176		T3
173		HK5

[illegible]

161-176 consensus

MSTnPKPQRkTKRNTnRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR

<u>SEQ</u>	<u>ID NO:</u>	<u>ISOLATE</u>
175		P8
170		IND8
162		S45
171		S9
163		D1
165		P10
169		IND3
164		US6
166		DK1
167		T10
168		SW2
161		SA10
174		HK4
172		HK3
176		T3
173		HK5

62 RQIPKARRPEGRAWAQPGHPWPLYaNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV  
62 RQIPKARRPEGRAWAQPGHPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV  
62 RQIPKARRPEGRAWAQPGHPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV  
62 RQIPKARhPEGRAWAQPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGpDPRRRSRNLGKV  
62 RQIPKARRPEGRAWAQPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV  
62 RQIPKARRPEGRAWAQPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV  
62 RQIPKARRPEGRAWAQPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV  
62 RQIPKARRPEGRAWAQPGYPWPLYGNEGMWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV  
62 RQIPKARRPEGRAWAQPGYPWPLYGNEGMWAGWLLSPRGSRPSWGpDPRRRSRNLGKV  
62 RQIPKARQPEGRAWAQPGYPWPLYGNEGMWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV  
62 RQIPKARQPEGRAWAQPGYPWPLYGNEGMWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV  
62 RQIPKARQPEGRtWAQPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV  
62 RQIPKARQPEGRtWAQPGYPWPLYGNEGMWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV  
62 RQIPKARQPEGRtWAQPGYPWPLYGNEGMWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV  
62 RQIPKARRPEGRaWAQPGYPWPLYGdEGMGWAGWLLSPRGSRPnWGPTDPRRRSRNLGKV  
62 RQIPKARRPEGRcWAQPGYPWPLYGnEGMGWAGWLLSPhGSRPsgWGPTDPRRRSRNLGKV

161-176      consensus

RQPIPKARrPEGRaWAQPgYPWPLYgnEG-GWAGWLLSPrGSRPsWGpTDPRRRSRNLGKV

<u>SEQ ID NO:</u>	<u>ISOLATE</u>
175	P8
170	IND8
162	S45
171	S9
163	D1
165	P10
169	IND3
164	US6
166	DK1
167	T10
168	SW2
161	SA10
174	HK4
172	HK3
176	T3
173	HK5

[illegible]

**161-176      consensus**

IDTLTCGFADLMGYIPLVGaPLGGaARALAHGVRVIEDGVNYATGNIPGc<sub>8</sub>FSIFLLALLS

<u>SEQ ID NO:</u>	<u>ISOLATE</u>
175	P8
170	IND8
162	S45

184 CLTiPASA  
184 CLTvPASA  
184 CLTiPASA



[illegible][illegible]

**MSTnPKPQRkTKRNTnRRPQDVKFPGGGOIVGGVYLLPRRGPRLGVRAtBKTSEERSOPRGR**

```

62 RQIPKARRPEGRtWAQPGYPWPLYGnEGMGWAGWLLSPhGSRPswGPTDPRRRSRNLGKV
62 RQIPKARRPEGRaWAQPGYPWPLYGdEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
62 RQIPKARQPEGRtWAQPGYPWPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
62 RQIPKARQPEGRtWAQPGYPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARQPEGRtWAQPGYPWPLYGnEGlGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARQPEGRaWAQPGYPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARQPEGRaWAQPGYPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRaWAQPGYPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRaWAQPGYPWPLYGnEGlGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRaWAQPGYPWPLYGnEGlGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRtWAQPGYPWPLYGnEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRtWAQPGYPWPLYGnEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRtWAQPGYPWPLYGnEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRtWAQPGYPWPLYGnEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRtWAQPGYPWPLYGnEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRaWAQPGHPWPLYGnEGlGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARhPEGRaWAQPGYPWPLYGnEGlGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARrPEGRaWAQPGHPWPLYaNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV

```

**RQPIPKARrPEGRaWAQPGyPWPLYgnEG-GWAGWLLSPrGSRP<sub>s</sub>WGPT<sub>t</sub>DPRRRSRNLGKV**

[illegible]

FIGURE 7C

159	S18	123	IDTLTCGFADLMGYIPLVGAPLGGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
160	DR4	123	IDTLTCGFADLMGYIPLVGAPLGGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
155	DK7	123	IDTLTCGFADLMGYIPLVGAPLGGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
170	IND8	123	IDTLTCGFADLMGYIPLVGAPLGGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
162	S45	123	IDTLTCGFADLMGYIPLVGAPLGGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
171	S9	123	IDTLTCGFADLMGYIPLVGAPLGGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
175	P8	123	IDTLTCGFADLMGYIPLVGgPLGGvARALAHGVRVvEDGVNYATGNLPGCSFSIFLLALLS

155-176	consensus	IDTLTCGFADLMGYIPLVGaPLGGaARALAHGVRVlEDGVNYATGNlPGCsFSIFLLALLS
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<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
173	HK5	184 CLTtPvSA
176	T3	184 CLTiPASA
172	HK3	184 CLTtPASA
174	HK4	184 CLTiPASA
161	SA10	184 CLTiPASA
168	SW2	184 CLTiPASA
167	T10	184 CLTiPASA
166	DK1	184 CLTiPASA
164	US6	184 CLTiPASA
169	IND3	184 CLTiPASA
165	P10	184 CLTiPASA
163	D1	184 CLTiPASA
156	US11	184 CLTVPASA
157	S14	184 CLTVPASA
158	SW1	184 CLTVPASA
159	S18	184 CLTVPASA
160	DR4	184 CLTVPASA
155	DK7	184 CLTVPASA
170	IND8	184 CLTVPASA
162	S45	184 CLTiPASA
171	S9	184 CLTiPASA
175	P8	184 CLTiPASA

155-176	consensus	CLTiPaSA
---------	-----------	----------

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FIGURE 7D

SEQ ID NO: ISOLATE  
179 T9  
178 US10  
180 T2  
177 T4

177-180 consensus

SEQ ID NO: ISOLATE  
179 T9  
178 US10  
180 T2  
177 T4

177-180 consensus

SEQ ID NO: ISOLATE  
179 T9  
178 US10  
180 T2  
177 T4

177-180 consensus

SEQ ID NO: ISOLATE  
179 T9  
178 US10  
180 T2  
177 T4

177-180 consensus

1 MSTNPKPQRKtiRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRtTRKTSERSQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR  
1 MSTiPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR  
1 MSTnPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR  
MSTnPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRaTRKTSERSQPRGR

62 RQIPKDRRsTGKSWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPsdPRHRSRNVGKV  
62 RQIPKDRRpTGKSWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPtDPRHRSRNVGKV  
62 RQIPKDRRSTGKSWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPNDPRHRSRNVGKV  
62 RQIPKDRRSTGKSWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPNDPRHRSRNVGKV  
RQIPKDRRsTGKSWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPnDPRHRSRNVGKV

123 IDTLTCGFADLMGYiPVVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS  
123 IDTLTCGFADLMGYiPVVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS  
123 IDTLTCGFADLMGYiPVVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS  
123 IDTLTCslADLMGYvPVVGgPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS  
IDTLTCgfADLMGYiPVVGaPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS

184 CITtPaSA  
184 CITIPVSA  
184 CITIPVSA  
184 CITIPVSA

CITiPvSA

0004691.05250.T6948000



FIGURE 7F

SEQ ID NO: ISOLATE

183 DK11  
184 SW3  
181 T8  
182 US1  
185 DK8  
186 S83  
178 US10  
180 T2  
179 T9  
177 T4

177-186 consensus

1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRtTRKTSERSQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRaTRKTSERSQPRGR

MSTnPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRaTRKtSESRQPRGR

SEQ ID NO: ISOLATE

183 DK11  
184 SW3  
181 T8  
182 US1  
185 DK8  
186 S83  
178 US10  
180 T2  
179 T9  
177 T4

177-186 consensus

62 RQPIPKDRRSTGKpWGKPGYPWPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHkSRNLGKV  
62 RQPIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHrSRNLGKV  
62 RQPIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHrSRNLGrV  
62 RQPIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHrSRNLGKV  
62 RQPIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHrSRNLGKV  
62 RQPIPKDRRtTGKsWGpPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRHkSRNLGKV  
62 RQPIPKDRRpTGKsWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRHkSRNLGKV  
62 RQPIPKDRRSTGKsWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRHrSRNVGKV  
62 RQPIPKDRRSTGKsWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRHrSRNVGKV  
62 RQPIPKDRRSTGKsWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRHrSRNVGKV  
62 RQPIPKDRRSTGKsWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRHrSRNVGKV

RQPIPKDRRsTGKsWGkPGYPWPLYGNEG-GWAGWLLSPRGsRpSwGPTDPRHrSRNLGkv

SEQ ID NO: ISOLATE

183 DK11  
184 SW3  
181 T8  
182 US1  
185 DK8  
186 S83  
178 US10  
180 T2  
179 T9  
177 T4

177-186 consensus

123 IDTITCGFADLMGYiPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS  
123 IDTITCGFADLMGYiPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS  
123 IDTITCGFADLMGYiPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS  
123 IDTITCGFADLMGYiPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS  
123 IDTITCGFADLMGYiPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS  
123 IDTLTCGFADLMGYiPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS  
123 IDTLTCGFADLMGYiPVVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS  
123 IDTLTCGFADLMGYiPVVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS  
123 IDTLTCGFADLMGYiPVVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS  
123 IDTLTCsLADLMGYvPVVGgPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS

IDT-TCGfADLMGYiPVVGaPvGGVARALAHGVRVLEDGiNYATGNLPGCSFSIFLLALLS

SEQ ID NO: ISOLATE

183 DK11  
184 SW3  
181 T8  
182 US1  
185 DK8  
186 S83  
178 US10  
180 T2  
179 T9  
177 T4

177-186 consensus

184 CcTVPVSA  
184 CFTVPVSA  
184 CFTVPVSA  
184 CaTVPVSA  
184 CcTVPVSA  
184 CIsVPVSA  
184 CITIPVSA  
184 CITIPVSA  
184 CITtPaSA  
184 CITiPvSA

CitvPvSA

FIGURE 7G

SEQ ID NO: ISOLATE  
189 S2  
187 HK10  
190 DK12  
188 S52

187-190 consensus

SEQ ID NO: ISOLATE  
189 S2  
187 HK10  
190 DK12  
188 S52

187-190 consensus

SEQ ID NO: ISOLATE  
189 S2  
187 HK10  
190 DK12  
188 S52

187-190 consensus

SEQ ID NO: ISOLATE  
189 S2  
187 HK10  
190 DK12  
188 S52

187-190 consensus

1 MSTLPPKQKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATRKTSESRQPRGR  
1 MSTLPPKQKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATRKTSESRQPRGR  
1 MSTLPPKQKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATRKTSESRQPRGR  
1 MSTLPPKQKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATRKTSESRQPRGR  
MSTLPPKQKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATRKTSESRQPRGR

62 RQIPKARRSEGRSWAQPYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV  
62 RQIPKARRSEGRSWAQPYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV  
62 RQIPKARRSEGRSWAQPYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV  
62 RQIPKARRSEGRSWAQPYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV  
RQIPKARRSEGRSWAQPYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV

123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS  
123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS  
123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS  
123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS  
IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS

184 CLHHPAAS  
184 CLHHPAAS  
184 CLHHPAAS  
184 CLVHPAAS

CLHHPAAS

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FIGURE 7H

SEQ ID NO: ISOLATE  
194 Z5  
193 Z1  
192 Z8  
195 Z6  
196 Z7  
191 Z4  
197 DK13

191-197 consensus

SEQ ID NO: ISOLATE  
194 Z5  
193 Z1  
192 Z8  
195 Z6  
196 Z7  
191 Z4  
197 DK13

191-197 consensus

SEQ ID NO: ISOLATE  
194 Z5  
193 Z1  
192 Z8  
195 Z6  
196 Z7  
191 Z4  
197 DK13

191-197 consensus

SEQ ID NO: ISOLATE  
194 Z5  
193 Z1  
192 Z8  
195 Z6  
196 Z7  
191 Z4  
197 DK13

191-197 consensus

1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRGR  
1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRaaRKTSEERSQPRGR  
1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRGR  
1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRGR  
1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRtTRKTSEERSQPRGR  
1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRGR  
1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSEERSQPRGR

MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRatRKTSEERSQPRGR

62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGqNDPRRRSRNLGKV  
62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDRRRSRNLGKV  
62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDRRRSRNLGKV  
62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDRRRSRNLGKV  
62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDRRRSRNLGKV  
62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDRRRSRNLGKV  
62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDRRRSRNLGKV  
62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDRRRSRNLGKV

RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGpNDPRRRSRNLGKV

123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINYATGNLPGCSFSIFLLALLS  
123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS  
123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS  
123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS  
123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINYATGNLPGCSFSIFLLALLS  
123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS  
123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINYATGNLPGCSFSIFLLALLS  
123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINYATGNLPGCSFSIFLLALLS

IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS

184 CLTTPASA  
184 CLTTPASA  
184 CLTVPASA  
184 CLTVPtSA  
184 CLTVPASA  
184 CLTVPASA  
184 CLTVPASA

CLTvPaSA

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FIGURE 71

SEQ ID NO: ISOLATE

205 SA11  
202 SA3  
198 SA4  
199 SA5  
200 SA7  
203 SA13  
201 SA1  
204 SA6

198-205 consensus

1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR  
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR

SEQ ID NO: ISOLATE

205 SA11  
202 SA3  
198 SA4  
199 SA5  
200 SA7  
203 SA13  
201 SA1  
204 SA6

198-205 consensus

62 RQIPKARQPTGRSWGQPGYPWPfYANEGLgWAGWLLSPRGSRPnWGPNDPRRrSRNLGKV  
62 RQIPKARQPTGRSWGQPGYPWPfYANEGLgWAGWLLSPRGSRPnWGPNDPRRrSRNLGKV  
62 RQIPKARQPTGRSWGQPGYPWPfYANEGLgWAGWLLSPRGSRPnWGPNDPRRrSRNLGKV  
62 RQIPKARQPTGRSWGQPGYPWPfYANEGLgWAGWLLSPRGSRPnWGPNDPRRrSRNLGKV  
62 RQIPKARQPTGRSWGQPGYPWPfYANEGLgWAGWLLSPRGSRPnWGPNDPRRrSRNLGKV  
62 RQIPKARQPTGRSWGQPGYPWPfYANEGLgWAGWLLSPRGSRPnWGPNDPRRrSRNLGKV  
62 RQIPKARQPTGRSWGQPGYPWPfYANEGLgWAGWLLSPRGSRPnWGPNDPRRrSRNLGKV  
62 RQIPKARQPTGRSWGQPGYPWPfYANEGLgWAGWLLSPRGSRPnWGPNDPRRrSRNLGKV  
62 RQIPKARQPTGRSWGQPGYPWPfYANEGLgWAGWLLSPRGSRPnWGPNDPRRrSRNLGKV  
62 RQIPKARQPTGRSWGQPGYPWPfYANEGLgWAGWLLSPRGSRPnWGPNDPRRrSRNLGKV

RQIPKARQPTGRSWGQPGYPWPfYANEGLgWAGWLLSPRGSRPnWGPNDPRRrSRNLGKV

SEQ ID NO: ISOLATE

205 SA11  
202 SA3  
198 SA4  
199 SA5  
200 SA7  
203 SA13  
201 SA1  
204 SA6

198-205 consensus

123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS  
123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS  
123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS  
123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS  
123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS  
123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS  
123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS  
123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS  
123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS  
123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS

IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS

SEQ ID NO: ISOLATE

205 SA11  
202 SA3  
198 SA4  
199 SA5  
200 SA7  
203 SA13  
201 SA1  
204 SA6

198-205 consensus

184 CLTVPaA  
184 CLTVPaA  
184 CLTVPaA  
184 CLTVPaA  
184 CLTVPaA  
184 CLTVPaA  
184 CLTVPaA  
184 CLTVPaA  
184 CLTVPaA  
184 CLTVPaA

CLTVPaA

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**FIGURE 7J**

SEQ ID NO:	Genotype	cons.
155-206	97	LLSPrGSRpSwGptDPRrrSRNlGkVIDTLTCgFADLMGyIPlVGaPlGGvArALAHGVRvLEDGvNyATGNlPGcAfSIFlLALLSCLtVpAaA
155-176	type 1	LLSPrGSRpSwGptDPRrrSRNlGkVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNIPGCASFIFLLALLSCLTIPaSA
177-186	type 2	LLSPRGSRpSwGptDPRHrSRNlGkVIDTLTCgFADLMGYIPlVGAPvGGVARALAHGVRVLEDGInYATGNlPGCSFSIFlLALLSCLtVpVpSA
187-190	type 3	LLSPRGSRpSwGPNDRPRrSRNlGkVIDTLTCGFADLMGYIPlVGAPvGGVARALAHGVRvLEDGInFATGNlPGCSFSIFlLALLSCLlHPAAS
191-197	type 4	LLSPRGSRpSwGPNDRPRrSRNlGkVIDTLTCGFADLMGYIPlVGAPvGGVARALAHGVRvLEDGInYATGNlPGCSFSIFlLALLSCLTIPaSA
198-205	type 5	LLSPRGSRpSwGPNDRPRrSRNlGkVIDTLTCGFADLMGYIPlVGPGvGGVARALAHGVRvLEDGVNYATGNlPGCSFSIFlLALLSCLtVpAaA
206	type 6	LLSPRGSRpSwGPNDRPRrSRNlGkVIDTLTCGFADLMGYIPlVGAPPLGGvAARALAHGVRvLEDGInYATGNlPGCSFSIFlLALLSCLTTPaSA

SEQ ID NO:	Genotype	10	20	30	40	50	60	70	80	90
155-160	I/1a	MSTNPKPARKTNRMTNTRPPDVKVFPFGGGLVGGVYLPRGPR	L	L	L	L	L	L	L	L
161-176	I/1b	---	K-K-NR-Q-V	---	L	---	L	---	L	---
177-180	III/2a	---	K-K-NR-Q-V	---	L	---	L	---	L	---
181-185	IV/2b	---	K-K-NR-Q-V	---	L	---	L	---	L	---
186	2c	---	K-K-NR-Q-V	---	L	---	L	---	L	---
187-190	(V)/3a	---	K-K-IR-Q-V	---	L	---	L	---	L	---
191	4a	---	K-K-NR-M-V	---	L	---	L	---	L	---
193	4b	---	K-K-NR-M-V	---	L	---	L	---	L	---
195	4c	---	K-K-NR-M-V	---	L	---	L	---	L	---
197	4d	---	K-K-NR-M-V	---	L	---	L	---	L	---
198	4e	---	K-K-NR-M-V	---	L	---	L	---	L	---
199	4f	---	K-K-NR-M-V	---	L	---	L	---	L	---
200	5a	---	K-K-NR-Q-V	---	L	---	L	---	L	---
201	5b	---	K-K-NR-Q-V	---	L	---	L	---	L	---
202	5c	---	K-K-NR-Q-V	---	L	---	L	---	L	---
203	5d	---	K-K-NR-Q-V	---	L	---	L	---	L	---
204	5e	---	K-K-NR-Q-V	---	L	---	L	---	L	---
205	5f	---	K-K-NR-Q-V	---	L	---	L	---	L	---
206	6a	---	K-K-NR-Q-V	---	L	---	L	---	L	---

SEQ ID NO:	Genotype	100	110	120	130	140	150	160	170	180	190
155-160	I/1a	LLSPGSRPaScptDPRRRN	LK	L-K	L-GF	L-L-A-L-A-R	VL	V-Y	L-S	L-L	L-LTV-ASA
161-176	I/11b	RR	RR	L-K	L-GF	L-L-A-L-A-R	VL	V-Y	L-S	L-L	L-LTI-ASA
177-180	III/2a	RR	RR	L-K	L-GF	L-L-A-L-A-R	VL	V-Y	L-S	L-L	L-LTI-VSA
181-185	I/2b	RR	RR	L-K	L-GF	L-L-A-L-A-R	VL	V-Y	L-S	L-L	L-LTV-VSA
186	2c	RR	RR	L-K	L-GF	L-L-A-L-A-R	VL	V-Y	L-S	L-L	L-LTV-VSA
187-190	(V)/3a	RR	RR	L-K	L-GF	L-L-A-L-A-R	VL	V-Y	L-S	L-L	L-LTV-VSA
191	4a	RR	RR	L-K	L-GF	L-L-A-L-A-R	VL	V-Y	L-S	L-L	L-LTV-VSA
193	4b	RR	RR	L-K	L-GF	L-L-A-L-A-R	VL	V-Y	L-S	L-L	L-LTV-VSA
195	4c	RR	RR	L-K	L-GF	L-L-A-L-A-R	VL	V-Y	L-S	L-L	L-LTV-VSA
197	4d	RR	RR	L-K	L-GF	L-L-A-L-A-R	VL	V-Y	L-S	L-L	L-LTV-VSA
194	4e	RR	RR	L-K	L-GF	L-L-A-L-A-R	VL	V-Y	L-S	L-L	L-LTV-VSA
192	4f	RR	RR	L-K	L-GF	L-L-A-L-A-R	VL	V-Y	L-S	L-L	L-LTV-VSA
198-205	5a	RR	RR	L-K	L-GF	L-L-A-L-A-R	VL	V-Y	L-S	L-L	L-LTV-VSA
206	6a	RR	RR	L-K	L-GF	L-L-A-L-A-R	VL	V-Y	L-S	L-L	L-LTV-VSA



